

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 1

722	752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA	
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser	
782	812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA	
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys	
842	872
Cadherin Cleavage	
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT	
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val	
902	932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG	
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys	
962	992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC	
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly	
1022	1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC	
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr	
1082	1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG	
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro	
1142	1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT	
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu	
1202	1232
Cadherin EC	
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG	
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg	
xxx	1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC	
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu	
1322	1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA	
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala	
1382	1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC	
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile	
1442	1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC	
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser	

FIG. 1 (cont.)

1502	1532
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC	
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn	
1562	1592
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA	
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser	
1622	1652
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT	
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp	
1682	1712
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA	
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln	
1742	1772
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT	
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile	
1802	1832
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT	
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe	
1862	1892
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC	
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val	
1922	1952
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG	
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu	
1982	2012
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA	
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly	
2042	2072
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC	
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his	
2102	2132
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT	
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala	
2162	2192
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC	
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn	
2222	2252
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG	
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu	
2282	2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG	

FIG. 1 (cont.)

cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 |xxxxxxxxxxxxxxxxxxxx Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xx|
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

3002 3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT

Fig. 1 (cont.)

cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

3182 3212
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu

3302 3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3422 3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln

3542 3572 |XXX
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met

3662 xxxxxxxxxxxxxxxxxxxxxxxxxxxx| 3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3782 3812 |xxxxxxxxxxxxxxxxxxxxx
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu

FIG. 1 (cont.)

arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

3902 xxx Coiled-Coil 2 xxxxxxxxxxxxxxxx 3932 xxxxx|

ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962

3992

AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022

|xxxx PBM xxxxx|

ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082

4112

TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142

4172

ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202

4232

TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262

4292

GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322

4352

CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382

4412

GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442

4472

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

Fig. 1 (cont.)

(Nucleotide position for insertions and deletion are found above the Human (h) CLASP-2A line diagram. Numbers are referenced based on hCLASP-2A nucleotide sequence from Figure 1.)

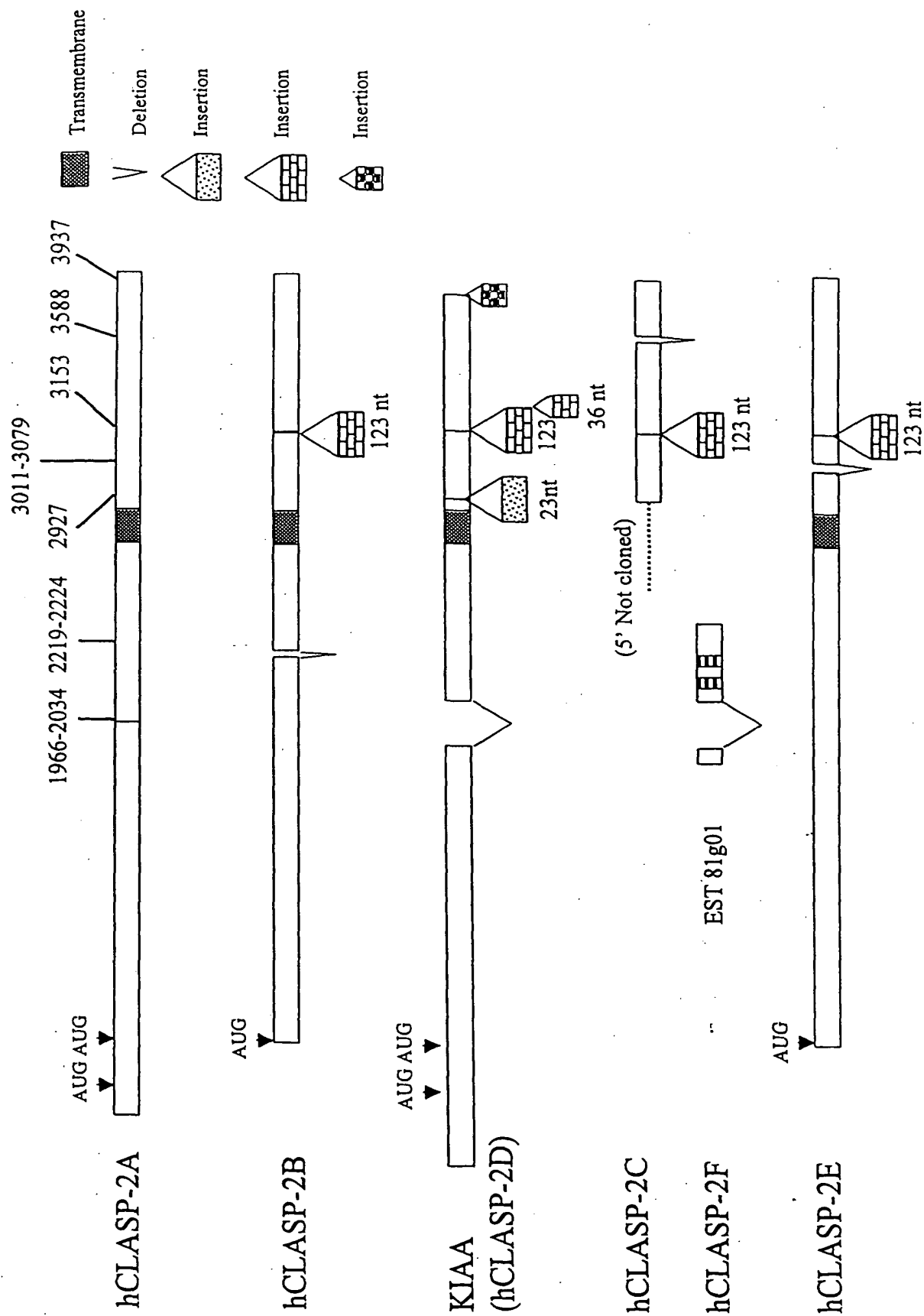


FIG. 2A

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr

362 392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 2B

722 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 872
|Cadherin Cleavage|
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly

1022 1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232 |Cadherin EC
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

xxx1 1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu

1322 1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

FIG. 2B (cont.)

1502	1532	
CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC		
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn		
1562	1592	
AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA		
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser		
1622	1652	
ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT		
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp		
1682	1712	
TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA		
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln		
1742	1772	
CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT		
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile		
1802	1832	
AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT		
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe		
1862	1892	
ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC		
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val		
1922	1952	1xxxxxxxxxxxxxxxxxxxxxx
TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG		
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu		
1982 xxxxxxxxxx	deleted in CLASP-2D(KIAA1058) xxxxxxxxxxxxxxxxxxxxxxxx1	
GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA		
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly		
2042	2072	
ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC		
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his		
2102	2132	
AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT		
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala		
		Deleted
2162	2192	1xxx
ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC		
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn		
in HC2B		
xxx1	2252	
CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG		
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu		

Fig. 2B (cont.)

2282 2312
TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 lxxxxxxxxxxxxxxxx Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

[Additional and differential exon usage found at position 2927 consisting of 69 nucleotides. This entire sequence is found in Human CLASP-2D (KIAA1058) and not other isoforms of CLASP-2. It has a sequence of:
AAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGGAGCCGGGGAG]

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|

TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu

Fig. 2B (cont.)

3602	3632
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA	
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys	
3662	3692
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT	
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr	
3722	3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG	
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu	
3782	3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA	
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu	
3842	3872
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA	
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu	
Insertion of 8 nucleotides found only in Human CLASP-2D with sequence: CTGGGATG	
3902	3932
ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG	
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr	
3962	3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA	
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr	
4022	1xxxx PBM xxxxi
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG	
met val his gly met thr ser ser ser ser val val STP	
4082	4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG	
4142	4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT	
4202	4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG	
4262	4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA	
4322	4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG	
4382	4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG	
4442	4472

FIG. 2B (cont.)

CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502

4532

GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562

4592

TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT

4622

4652

GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682

4712

TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742

4772

ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802

TTT ACT

Fig. 2B (cont.)

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAAT
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTTCGGAAACCTGAGAAGATG
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCTAAGCTCCCAAGTGATTTTAGGCAATCTAGACATTACAATTGATAATGTTTCCTCAGAC
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTCCCTAATTATGTTAATTCATCATAATTCCCACAAAACAATTTGAAACCTGCAGTAAA
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ACTCCCATCACGTTTGAAGTGGAGGAATTTGTGCCCTGCATACCAAAACACACTCAGCCT
HC2E	-----
HC2F	-----

FIG. 3A

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TACACCATCTACACCAATCACCTTTACGTTTATCCTAAGTACTTGAAATACGACAGTCAG
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTCTTTTGCCAAGGCTAGAAATATTGCGATTTCATTGAATTCAAAGATTCAGATGAG
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GAAGACTCTCAGCCCCTTAAGTGCATTTATGGCAGACCTGGTGGGCCAGTTTTTACAAGA
HC2E	-----
HC2F	-----

HC2A	-----AGTTTTACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAA
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCGCCTTTGCTGCAGTTTTACACCATCACCAAAACCCAGAATTTTATGATGAGATTAAA
HC2E	-----
HC2F	-----

HC2A	ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATAGAGTTGCCCACTCAGCTGCATGAAAAGCACCACCTGTTGCTCACATTCTTCCATGTC
HC2E	-----
HC2F	-----

HC2A	AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCTGTGACAACTCAAGTAAAGGAAGCACGAAGAAGAGGGATGTCGTTGAAACCCAAGTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	GGCTACTCCTGGCTTCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GGCTACTCCTGGCTTCCCTCCTGAAAGACGGAAGGGTGGTGACAAGCGAGCAGCACATC
HC2E	-----
HC2F	-----

HC2A	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAAGAGCTTGGGATGGGCAGG
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCGGTCTCGGCGAACCTTCCTTCGGGCTATCTTGGCTACCAGGAGCTTGGGATGGGCAGG
HC2E	-----
HC2F	-----

HC2A	CATTATGGTCCGGAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATTATGGTCCGGAATTAAATGGGTAGATGGAGGCAAGCCACTGCTGAAAATTTCCACT
HC2E	-----
HC2F	-----

HC2A	CATCTGGTTTCTACAGTGATACTCAGGATCAGCATTTACATAATTTTCCAGTACTGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CATCTGGTTTCTACAGTGATACTCAGGATCAGCATTTACATAATTTTCCAGTACTGT
HC2E	-----
HC2F	-----

HC2A	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACCTTGTAAGTACCTTAAGAGT
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CAGAAAACCGAATCTGGAGCCCAAGCCTTAGGAAACGAACCTTGTAAGTACCTTAAGAGT
HC2E	-----
HC2F	-----

HC2A	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2-80	-----
HC2B	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2C	-----
HC2D-KIAA1058	CTGCATGCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2E	-----GCGATGGAAGGCCACGTGATGATCGCCTTCTTGCCCACTATCCTAAACCAGCTG
HC2F	-----

Fig. 3A (cont.)

HC2A	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2-80	-----
HC2B	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2C	-----
HC2D-KIAA1058	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2E	TTCCGAGTCCTCACCAGAGCCACACAGGAAGAAGTCGCGGTTAACGTGACTCGGGTCATT
HC2F	-----

HC2A	ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2-80	-----
HC2B	ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2C	-----
HC2D-KIAA1058	ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2E	ATTCATGTGGTTGCCAGTGCCATGAGGAAGGATTGGAGAGCCACTTGAGGTCATATGTT
HC2F	-----

HC2A	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2-80	-----
HC2B	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2C	-----
HC2D-KIAA1058	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2E	AAGTACGCGTATAAGGCTGAGCCATATGTTGCCTCTGAATACAAGACAGTGCATGAAGAA
HC2F	-----

HC2A	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA
HC2-80	-----
HC2B	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA
HC2C	-----
HC2D-KIAA1058	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA
HC2E	CTGACCAAATCCATGACCACGATTCTCAAGCCTTCTGCCGATTTCTCACCAGCAACAAA
HC2F	-----

HC2A	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2-80	-----
HC2B	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2C	-----
HC2D-KIAA1058	CTACTGAAGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2E	CTACTGAGGTACTCATGGTTTTTCTTTGATGTACTGATCAAATCTATGGCTCAGCATTTG
HC2F	-----

HC2A	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTGCATCCTATCATCAT
HC2-80	-----
HC2B	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTGCATCCTATCATCAT
HC2C	-----
HC2D-KIAA1058	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTGCATCCTATCATCAT
HC2E	ATAGAGAACTCCAAAGTTAAGTTGCTGCGAAACCAGAGATTTCTGCATCCTATCATCAT
HC2F	-----

Fig. 3A (cont.)

HC2A	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2-80	-----
HC2B	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2C	-----
HC2D-KIAA1058	GCAGTGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2E	GCAGCGGAAACCGTTGTAAATATGCTGATGCCACACATCACTCAGAAGTTTGGAGATAAT
HC2F	-----

HC2A	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2-80	-----
HC2B	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2C	-----
HC2D-KIAA1058	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2E	CCAGAGGCATCTAAGAACGCGAATCATAGCCTTGCTGTCTTCATCAAGAGATGTTTCACC
HC2F	-----

HC2A	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACTACATTAGCTGTTTTGCTCCT
HC2-80	-----
HC2B	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACTACATTAGCTGTTTTGCTCCT
HC2C	-----
HC2D-KIAA1058	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACTACATTAGCTGTTTTGCTCCT
HC2E	TTCATGGACAGGGGCTTTGTCTTCAAGCAGATCAACAACACTACATTAGCTGTTTTGCTCCT
HC2F	-----

HC2A	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2-80	-----
HC2B	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2C	-----
HC2D-KIAA1058	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2E	GGAGACCCAAAGACCCTCTTTGAATACAAGTTTGAATTTCTCCGTGTAGTGTGCAACCAT
HC2F	-----

HC2A	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2-80	-----
HC2B	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2C	-----
HC2D-KIAA1058	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2E	GAACATTATATTCCGTTGAACTTACCAATGCCATTTGGAAAAGGCAGGATTCAAAGATAC
HC2F	-----

HC2A	CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2-80	-----TCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2B	CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2C	-----
HC2D-KIAA1058	CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2E	CAAGACCTCCAGCTTGACTACTCATTAACAGATGAGTTCTGCAGAAACCACTTCTTGGTG
HC2F	-----

HC2A	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2-80	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2B	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2C	-----
HC2D-KIAA1058	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2E	GGACTGTTACTGAGGGAGGTGGGGACAGCCCTCCAGGAGTTCCGGGAGGTCCGTCTGATC
HC2F	-----
HC2A	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2-80	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2B	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2C	-----
HC2D-KIAA1058	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2E	GCCATCAGTGTGCTCAAGAACCTGCTGATAAAGCATTCTTTTGATGACAGATATGCTTCA
HC2F	-----
HC2A	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2-80	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2B	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2C	-----
HC2D-KIAA1058	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2E	AGGAGCCATCAGGCAAGGATAGCCACCCTCTACCTGCCTCTGTTTGGTCTGCTGATTGAA
HC2F	-----
HC2A	AACGTCCAGCGGATCAATGTGAGGGATGTGTCAACCCTTCCCTGTGAACGCGGGCATGACC
HC2-80	AACGTCCAGCGGATCAATGTGAGGGATGTGTCAACCCTTCCCTGTGAACGCGGGCATGACC
HC2B	AACGTCCAGCGGATCAATGTGAGGGATGTGTCAACCCTTCCCTGTGAACGCGGGCATGACC
HC2C	-----
HC2D-KIAA1058	AACGTCCAGCGGATCAATGTGAGGGATGTGTCAACCCTTCCCTGTGAACGCGGGCATGACC
HC2E	AACGTCCAGCGGATCAATGTGAGGGATGTGTCAACCCTTCCCTGTGAACGCGGGCATGACC
HC2F	-----
HC2A	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2-80	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2B	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2C	-----
HC2D-KIAA1058	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2E	GTGAAGGATGAATCCCTGGCTCTACCAGCTGTGAATCCGCTGGTGACGCCGAGAAAGGGA
HC2F	-----
HC2A	AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2-80	AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2B	AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2C	-----
HC2D-KIAA1058	AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2E	AGCACCTGGACAACAGCCTGCACAAGGACCTGCTGGGCGCCATCTCCGGCATTGCTTCT
HC2F	-----

Fig. 3A (cont.)

HC2A	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2-80	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2B	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2C	-----
HC2D-KIAA1058	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2E	CCATATACAACCTCAACTCCAAACATCAACAGTGTGAGAAATGCTGATTTCGAGAGGATCT
HC2F	-----GCTGATTTCGAGAGGATCT

HC2A	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2-80	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2B	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2C	-----
HC2D-KIAA1058	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2E	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC
HC2F	CTCATAAGCACAGATTTCGGGTAACAGCCTTCCAGAAAGGAATAGTGAGAAGAGCAATTCC

HC2A	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2-80	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2B	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2C	-----
HC2D-KIAA1058	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2E	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT
HC2F	CTGGATAAGCACCAACAAAGTAGCACATTGGGAAATTCCGTGGTTCGCTGTGATAAACTT

HC2A	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2-80	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2B	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2C	-----
HC2D-KIAA1058	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2E	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT
HC2F	GACCAGTCTGAGATTAAGAGCCTACTGATGTGTTTCCTCTACATCTTAAAGAGCATGTCT

HC2A	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2-80	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2B	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2C	-----
HC2D-KIAA1058	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2E	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT
HC2F	GATGATGCTTTGTTTACATATTGGAACAAGGCTTCAACATCTGAACCTTATGGATTTTTTT

HC2A	ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG
HC2-80	ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG
HC2B	ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG
HC2C	-----
HC2D-KIAA1058	ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG
HC2E	ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG
HC2F	ACAATATCTGAAGTCTGCCTGCACCAGTTCAGTACATGGGGAAGCGATACATAGCCAGG

Fig. 3A (cont.)

HC2A	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2-80	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2B	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2C	-----
HC2D-KIAA1058	-----AA-----
HC2E	AACCAGGAGGGGTTGGGACCCATAGTTCATGATCGAAAGTCTCAGACATTGCCTGTTTCC
HC2F	-----TGTGA-----GAAAG-----ATATCAAGTGT-----

HC2A	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2-80	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2B	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2C	-----
HC2D-KIAA1058	-----CAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2E	CGTAACAGAACAGGAATGATGCATGCCAGATTGCAGCAGCTGGGCAGCCTGGATAACTCT
HC2F	-----GCTTGGAA-----

HC2A	CTCACTTTTAAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2-80	CTCACTTTTAAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2B	CTCACTTTTAAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2C	-----
HC2D-KIAA1058	CTCACTTTTAAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2E	CTCACTTTTAAACCACAGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT
HC2F	-TTTCTGTAGACAATGGCTATGGCCACTCGGACGCAGATGTTCTGCACCAGTCATTACTT

HC2A	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2-80	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2B	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2C	-----
HC2D-KIAA1058	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2E	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA
HC2F	GAAGCCAACATTGCTACTGAGGTTTGCCTGACAGCTCTGGACACGCTTTCTCTATTTACA

HC2A	TTGGCGTTTAAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2-80	TTGGCGTTTAAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2B	TTGGCGTTTAAAG-----CTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2C	-----
HC2D-KIAA1058	TTGGCGTTTAAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2E	TTGGCGTTTAAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT
HC2F	TTGGCGTTTAAAGAACCAGCTCCTGGCCGACCATGGACATAATCCTCTCATGAAAAAAGTT

HC2A	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2-80	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2B	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2C	-----
HC2D-KIAA1058	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2E	TTTGATGTCTACCTGTGTTTTCTTCAAAAACATCAGTCTGAAACGGCTTTAAAAAATGTC
HC2F	A-----

Fig. 3A (cont.)

HC2A	TTCAC	TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2-80	TTCAC	TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2B	TTCAC	TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2C	-----	-----
HC2D-KIAA1058	TTCAC	TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2E	TTCAC	TGCCTTAAGGTCCTTAATTTATAAGTTTCCCTCAACATTCTATGAAGGGAGAGCG
HC2F	-----	-----

HC2A	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTA	ACTCCAAGCTGAGCTCC
HC2-80	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTA	ACTCCAAGCTGAGCTCC
HC2B	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTA	ACTCCAAGCTGAGCTCC
HC2C	-----	-----
HC2D-KIAA1058	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTA	ACTCCAAGCTGAGCTCC
HC2E	GACATGTGTGCGGCTCTGTGTTACGAGATTCTCAAGTGCTGTA	ACTCCAAGCTGAGCTCC
HC2F	-----	-----

HC2A	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACA	ACTTTGATTACACT
HC2-80	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACA	ACTTTGATTACACT
HC2B	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACA	ACTTTGATTACACT
HC2C	-----	-----
HC2D-KIAA1058	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACA	ACTTTGATTACACT
HC2E	ATCAGGACGGAGGCCTCCAGCTGCTCTACTTCCTGATGAGGAACA	ACTTTGATTACACT
HC2F	-----	-----

HC2A	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGT	CAGCCAGCTGATA
HC2-80	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGT	CAGCCAGCTGATA
HC2B	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGT	CAGCCAGCTGATA
HC2C	-----	-----
HC2D-KIAA1058	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGT	CAGCCAGCTGATA
HC2E	GGAAAGAAGTCCTTTGTCCGGACACATTTGCAAGTCATCATATCTGT	CAGCCAGCTGATA
HC2F	-----	-----

HC2A	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2-80	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2B	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2C	-----
HC2D-KIAA1058	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2E	GCAGACGTTGTTGGCATTGGGGAAACCAGATTCCAGCAGTCCCTGTCCATCATCAACAAC
HC2F	-----

HC2A	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2-80	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2B	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2C	-----
HC2D-KIAA1058	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2E	TGTGCCAACAGTGACCGGCTTATTAAGCACACCAGCTTCTCCTCTGATGTGAAGGACTTA
HC2F	-----

FIG. 3A (cont.)

HC2A	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2-80	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2B	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2C	-----
HC2D-KIAA1058	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2E	ACCAAAAGGATACGCACGGTGCTAATGGCCACCGCCCAGATGAAGGAGCATGAGAACGAC
HC2F	-----
HC2A	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2-80	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2B	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2C	-----
HC2D-KIAA1058	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2E	CCAGAGATGCTGGTGGACCTCCAGTACAGCCTGGCCAAATCCTATGCCAGCACGCCCCGAG
HC2F	-----
HC2A	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2-80	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2B	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2C	-----
HC2D-KIAA1058	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2E	CTCAGGAAGACGTGGCTCGACAGCATGGCCAGGATCCATGTCAAAAATGGCGATCTCTCA
HC2F	-----
HC2A	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCCTAGTGGCAGAATATCTCACACGGAAA
HC2-80	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCCTAGTGGCAGAATATCTCACACGGAAA
HC2B	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCCTAGTGGCAGAATATCTCACACGGAAA
HC2C	-----
HC2D-KIAA1058	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCCTAGTGGCAGAATATCTCACACGGAAA
HC2E	GAGGCAGCAATGTGCTATGTCCACGTAACAGCCCCTAGTGGCAGAATATCTCACACGGAAA
HC2F	-----
HC2A	G-----
HC2-80	G-----
HC2B	G-----
HC2C	-----
HC2D-KIAA1058	GAAGCAGTCCAGTGGGAGCCGCCCTTCTCCCCACAGCCATAGCGCCTGCCTGAGGAGG
HC2E	G-----
HC2F	-----
HC2A	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2-80	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2B	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2C	-----GTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2D-KIAA1058	AGCCGGGGAGGCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2E	-----GCGTGTTTAGACAAGGATGCACCGCCTTCAGGGTCATTACCCCAAACATC
HC2F	-----

Fig. 3A (cont.)

HC2A	GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2-80	GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2B	GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2C	GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2D-KIAA1058	GACGAGGAGGCCTCCATGATGGAAGACGTGGGGATGCAGGATGTCCATTTCAACGAGGAT
HC2E	GACGAGGAGGCCTCCATGATGGAAGACGTGGGGA-----
HC2F	-----

HC2A	GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2-80	GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2B	GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2C	GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2D-KIAA1058	GTGCTGATGGAGCTCCTTGAGCAGTGCGCAGATGGACTCTGGAAAGCCGAGCGCTACGAG
HC2E	-----AAGCCGAGCGCTACGAG
HC2F	-----

HC2A	CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTT----
HC2-80	CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTT----
HC2B	CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2C	CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2D-KIAA1058	CTCATTGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2E	CTCATCGCCGACATCTACAAACTTATCATCCCCATTTATGAGAAGCGGAGGGATTTTGAG
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2C	AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2D-KIAA1058	AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2E	AGGCTGGCCCATCTGTATGACACGCTGCACCGGGCCTACAGCAAAGTGACCGAGGTCATG
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
HC2C	CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
HC2D-KIAA1058	CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGGCAGG
HC2E	CACTCGGGCCGAGGCTTCTGGGGACCTACTTCCGGGTAGCCTTCTTCGGGCAGG----
HC2F	-----

HC2A	-----CTTTGAAGATGAAGATGGA
HC2-80	-----CTTTGAAGATGAAGATGGA
HC2B	-----GATTCTTTGAAGATGAAGATGGA
HC2C	-----GATTCTTTGAAGATGAAGATGGA
HC2D-KIAA1058	CAATACCAGTTTACAGACAGTGAAACAGATGTGGAGGGATTCTTTGAAGATGAAGATGGA
HC2E	-----GATTCTTTGAAGATGAAGATGGA
HC2F	-----

Fig. 3A (cont.)

HC2A	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTGGAAATTTCTCAGAGACTC
HC2-80	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTGGAAATTTCTCAGAGACTC
HC2B	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTGGAAATTTCTCAGAGACTC
HC2C	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTGGAAATTTCTCAGAGACTC
HC2D-KIAA1058	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTGGAAATTTCTCAGAGACTC
HC2E	AAGGAGTATATTTACAAGGAACCCAAACTCACACCGCTGTCTGGAAATTTCTCAGAGACTC
HC2F	-----

HC2A	CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2-80	CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2B	CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2C	CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2D-KIAA1058	CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2E	CTTAAACTGTACTCGGATAAATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGC
HC2F	-----

HC2A	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2-80	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2B	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2C	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2D-KIAA1058	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCCTACATCCAGGTGACTCACGTCATC
HC2E	AAGGTCAACCCTAAGGATCTGGATTCTAAGTATGCATACATCCAGGTGACTCACGTCATC
HC2F	-----

HC2A	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC
HC2-80	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC
HC2B	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC
HC2C	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC
HC2D-KIAA1058	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC
HC2E	CCCTTCTTTGACGAAAAAGAGTTGCAAGAAAGGAAAAACAGAGTTTGAGAGATCCCACAAC
HC2F	-----

HC2A	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2-80	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2B	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2C	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2D-KIAA1058	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2E	ATCCGCCGCTTCATGTTTGAGATGCCATTTACGCAGACCGGGAAGAGGCAGGGCGGGGTG
HC2F	-----

HC2A	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2-80	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2B	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2C	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2D-KIAA1058	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2E	GAAGAGCAGTGCAAACGGCGCACCATCCTGACAGCCATACACTGCTTCCCTTATGTGAAG
HC2F	-----

Fig. 3A (cont.)

HC2A	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2-80	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2B	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2C	AAGCGCATCCCTTTTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGT--CCATT
HC2D-KIAA1058	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2E	AAGCGCATCCCTGTCATGTACCAGCACCACACTGACCTGAACCCCATCGAGGTGGCCATT
HC2F	-----

HC2A	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2-80	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2B	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2C	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2D-KIAA1058	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2E	GACGAGATGAGTAAGAAGGTGGCGGAGCTCCGGCAGCTGTGCTCCTCGGCCGAGGTGGAC
HC2F	-----

HC2A	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2-80	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2B	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2C	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2D-KIAA1058	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2E	ATGATCAAACCTGCAGCTCAAACCTCCAGGGCAGCGTGAGTGTTCAAGTCAATGCTGGCCCA
HC2F	-----

HC2A	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2-80	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2B	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2C	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2D-KIAA1058	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2E	CTAGCATATGCGCGAGCTTTCTTAGATGATACAAACACAAAGCGATATCCTGACAATAAA
HC2F	-----

HC2A	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2-80	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2B	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2C	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2D-KIAA1058	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2E	GTGAAGCTGCTTAAGGAAGTTTTTCAGGCAATTTGTGGAAGCTTGCGGTCAAGCCTTAGCG
HC2F	-----

HC2A	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2-80	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2B	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2C	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2D-KIAA1058	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2E	GTAAACGAACGTCTGATTAAAGAAGACCAGCTCGAGTATCAGGAAGAAATGAAAGCCAAC
HC2F	-----

FIG. 3A (cont.)

HC2A	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2-80	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2B	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2C	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2D-KIAA1058	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAGCTGGGATGATCTGCC
HC2E	TACAGGGAAATGGCGAAGGAGCTTTCTGAAATCATGCATGAGCAG-----ATCTGCC
HC2F	-----

HC2A	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2-80	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2B	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2C	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2D-KIAA1058	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2E	CCCTGGAGGAGAAGACGAGCGTCTTACCGAATTCCCTTCACATCTTCAACGCCATCAGTG
HC2F	-----

HC2A	GGACTCCAACAAGCACAATGGTTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2-80	GGACTCCAACAAGCACAATGGTTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2B	GGACTCCAACAAGCACAATGGTTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2C	GGACTCCAACAAGCACAATGGTTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2D-KIAA1058	GGACTCCAACAAGCACAATGGTTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2E	GGACTCCAACAAGCACAATGGTTTACGGGATGACCAGCTCGTCTTCGGTCGTGTGATTAC
HC2F	-----

HC2A	ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTGATTTGCAAACCTCAGGATGCTTTCCAA
HC2-80	ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTGATTTGCAAACCTCAGGATGCTTTCCAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATCTCATGGCCCGTGTGTGGGGACTTGCTTTGTGATTTGCAAACCTCAGGATGCTTTCCAA
HC2E	-----
HC2F	-----

HC2A	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2-80	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCAAGGGGAAGGGGAGAGAAAGGAAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGCCAATCACTGGGGAGACCGAGCACAGGGAGGACCA - GGGGAAGGGGAGAGAAAGGAAA
HC2E	-----
HC2F	-----

HC2A	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2-80	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAGAACAACGTTATTTCTTAACAGACTTTCTATAGGAGTTGTAAGAAGGTGCACATAT
HC2E	-----
HC2F	-----

Fig. 3A (cont.)

HC2A	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2-80	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTTTTAAATCTCACTGGCAATATTCAAAGTTTTTCATTGTGTCTTAACAAAGGTGTGGTA
HC2E	-----
HC2F	-----

HC2A	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2-80	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GACACTCTTGAGCTGGACTTAGATTTTATTCTTCCTTGCAGAGTAGTGTTAGAATAGATG
HC2E	-----
HC2F	-----

HC2A	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2-80	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTACAGAAAAAAGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGAT
HC2E	-----
HC2F	-----

HC2A	GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGAAATCTGATCGTAATCAGGGTACAGAA
HC2-80	GCCTGGGGGACCTTTTGCCTCGACTCGTGCCGAAATCTGATCGTAATCAGGGTACAGAA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	GCCTGGGGGACCTTTTGCCTCGAGGCTGAGCTGGAAATCTTGAAATATTTTTTT---T
HC2E	-----
HC2F	-----

HC2A	CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2-80	CTTACTAGTTTTGTCTAGGAGTATGTTGTATGACTAGGATTTGTGCTATTATCTCATTCA
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTCCTGTGGCACATTCAGGTTGAATACAAGAACTATTTTTGTGACTAGTTTTTGTATGAC
HC2E	-----
HC2F	-----

HC2A	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2-80	ACAACATAGAGCAAGAATAGTGAGCTAACTGAGCTAGACACTCAATTAATCCGCTACTGG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CTAAGGGAAGTACCATTGTAATTTTTGTACCAGTGAACCAGGAGATTAGTGCTTTTAT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	CTTCAAGTCAGAACTTTGTCTTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2-80	CTTCAAGTCAGAACTTTGTCTTAATCATCGACTCCGGGACGGTCATATATGTATTACAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATTCATTTTCCTTGCAATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAACT
HC2E	-----
HC2F	-----

HC2A	TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2-80	TTCTACATTTTTAATACTCACATGGGCTTATGCATTAAGTTTAATTGTGATAAATTTGTG
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AGTCAAGCAGTTTAGAACCAAAGGCCTATATTAATAACCGCAACTATGCTGAAAAGTACA
HC2E	-----
HC2F	-----

HC2A	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTGCATAAAAATGTGCAATAT
HC2-80	CTGGTCCAGTATATGCAATACACTTTAATGGTTTATTCTTGTGCATAAAAATGTGCAATAT
HC2B	-----
HC2C	-----
HC2D-KIAA1058	AAGTAGTACAGTATATTGTTATGTACATATCATTGTTAATACAGTCCTGGCATTCTGTAC
HC2E	-----
HC2F	-----

HC2A	GGAGATGTATACAAGTCTTTACT-----
HC2-80	GGAGATGTATACAAGTCTTTACT-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	ATATATGTATTACATTTCTACATTTTAATACTCACATGGGCTTATGCATTAAGTTTAAT
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGTGATAAATTTGTGCTGTTCCAGTATATGCAATACACTTTAATGTTTTATTCTTGTACA
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAAAATGTGCAATATGGAGATGTATACAGTCTTTACTATATTAGGTTTATAAACAGTTT
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TAAGAATTTTCATCCTTTTGCCAAAATGGTGGAGTATGTAATTGGTAAATCATAAATCCTG
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TGGTGAATGGTGGTGTACTTTAAAGCTGTCACCATGTTATATTTTCTTTTAAGACATTAA
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	TTTAGTAATTTTATATTTGGGAAAATAAAGGTTTTTAATTTTATTTAACTGGAATCACTG
HC2E	-----
HC2F	-----

HC2A	-----
HC2-80	-----
HC2B	-----
HC2C	-----
HC2D-KIAA1058	CCCTGCTGTAATTAAACATTCTGTACCACATCTGTATTAAAAAGACATTGCTGACC
HC2E	-----
HC2F	-----

FIG. 3A (cont.)

HC2A	-----
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
HC2E	-----
HC2F	-----

HC2A	-----
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
HC2E	-----
HC2F	-----

HC2A	-----VLHHHQNPEFYDEIK
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	XSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
HC2E	-----
HC2F	-----

HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC2E	-----
HC2F	-----

HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
HC2A-80	-----
HC2B	-----
HC2C	-----
HC2D	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
HC2E	-----
HC2F	-----

HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2A-80	-----
HC2B	-----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2C	-----
HC2D	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2E	-----AMEGHVMIAFLPTILNQLFRVLTRATQEEVAVNVTRVI
HC2F	-----

Fig. 3B

HC2A	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2A-80	-----
HC2B	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2C	-----
HC2D	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2E	IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSNK
HC2F	-----

HC2A	LLRYSWFFFDFVLIKSMQHLIENSKVKLLRNQRFPAZYHHAETVVNMLMPHITQKFGDN
HC2A-80	-----
HC2B	LLRYSWFFFDFVLIKSMQHLIENSKVKLLRNQRFPAZYHHAETVVNMLMPHITQKFGDN
HC2C	-----
HC2D	LLKYSWFFFDFVLIKSMQHLIENSKVKLLRNQRFPAZYHHAETVVNMLMPHITQKFRDN
HC2E	LLRYSWFFFDFVLIKSMQHLIENSKVKLLRNQRFPAZYHHAETVVNMLMPHITQKFGDN
HC2F	-----

HC2A	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2A-80	-----
HC2B	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2C	-----
HC2D	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2E	PEASKNANHSLAVFIKRCFTFMDRGFVFKQINNYISCFAPGDPKTLFEYKFEFLRVVCNH
HC2F	-----

HC2A	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2A-80	-----QLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2B	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2C	-----
HC2D	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2E	EHYIPLNLPMPFGKGRIQRYQDLQLDYSLTDEFCRNHFLVGLLLREVGTLQEFREVRLI
HC2F	-----

HC2A	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2A-80	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2B	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2C	-----
HC2D	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2E	AISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVQRINVRDVSPFPVNAGMT
HC2F	-----

HC2A	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2A-80	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2B	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2C	-----
HC2D	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2E	VKDESLALPAVNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTTSTPNINSVRNADSRGS
HC2F	-----ADSRGS

HC2A	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2A-80	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2B	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2C	-----
HC2D	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2E	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS
HC2F	LISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSEIKSLLMCFLYILKSMS

HC2A	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGGLGPIVHDRKSQTL PVS
HC2A-80	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGGLGPIVHDRKSQTL PVS
HC2B	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGGLGPIVHDRKSQTL PVS
HC2C	-----
HC2D	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIAR-----
HC2E	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIARNQEGGLGPIVHDRKSQTL PVS
HC2F	DDALFTYWNKASTSELMDFFTISEVCLHQFQYMGKRYIAS-----VR--KISSVLGIS

HC2A	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2A-80	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2B	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2C	-----
HC2D	---TGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2E	RNRTGMMHARLQQLGSLDNSLTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFT
HC2F	V-----D-NG-----YGHSDADVLHQSLLEANIATEVCLTALDTLSLFT

HC2A	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA
HC2A-80	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA
HC2B	LAFK--LLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA
HC2C	-----
HC2D	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA
HC2E	LAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIYKFPSTFYEGRA
HC2F	LAFKNQLLADHGHNPMLKKK-----

HC2A	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQ LI
HC2A-80	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQ LI
HC2B	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQ LI
HC2C	-----
HC2D	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQ LI
HC2E	DMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTHLQVIIISVSQ LI
HC2F	-----

HC2A	ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2A-80	ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2B	ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2C	-----
HC2D	ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2E	ADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKEHEND
HC2F	-----

HC2A	PEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNLSEAMCYVHVLTALVAEYLTRK
HC2A-80	PEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNLSEAMCYVHVLTALVAEYLTRK
HC2B	PEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNLSEAMCYVHVLTALVAEYLTRK
HC2C	-----
HC2D	PEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNLSEAMCYVHVLTALVAEYLTRK
HC2E	PEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNLSEAMCYVHVLTALVAEYLTRK
HC2F	-----

HC2A	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2A-80	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2B	-----GVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2C	-----FRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2D	EAVQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPNIDEEASMMEDVGMQDVHFNE
HC2E	-----GVFRQGCTAFRVITPNIDEEASMMEDVG-----
HC2F	-----

HC2A	DVLMELLEQCADGLWKAERYELIADIYKLIPIYEKRR-----
HC2A-80	DVLMELLEQCADGLWKAERYELIADIYKLIPIYEKRR-----
HC2B	DVLMELLEQCADGLWKAERYELIADIYKLIPIYEKRRDFERLAHLYDTLHRAYSK
HC2C	DVLMELLEQCADGLWKAERYELIADIYKLIPIYEKRRDFERLAHLYDTLHRAYSK
HC2D	DVLMELLEQCADGLWKAERYELIADIYKLIPIYEKRRDFERLAHLYDTLHRAYSK
HC2E	-----KAERYELIADIYKLIPIYEKRRDFERLAHLYDTLHRAYSK
HC2F	-----

HC2A	-----DFFEDEDGKEYIYKEPKLTPLE
HC2A-80	-----DFFEDEDGKEYIYKEPKLTPLE
HC2B	VTEVMHSGRRLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPLE
HC2C	VTEVMHSGRRLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPLE
HC2D	VTEVMHSGRRLGTYFRVAFFGQAQYQFTDSETDVEGFFEDEDGKEYIYKEPKLTPLE
HC2E	VTEVMHSGRRLGTYFRVAFFGQ-----GFFEDEDGKEYIYKEPKLTPLE
HC2F	-----

HC2A	ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2A-80	ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2B	ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2C	ISQRLKLYSDKFGSENVKMTQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2D	ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2E	ISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIPFFDEKELQERKTEF
HC2F	-----

HC2A	ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2A-80	ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2B	ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2C	ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2D	ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2E	ERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTAIHCFPYVKKRIPVMYQHHTDLNP
HC2F	-----

HC2A	IEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2A-80	IEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2B	IEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2C	IEVHZ-----
HC2D	IEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2E	IEVAIDEMSKKVAELRQLC SSAEVDMIKLQLKLQGSVSVQVNAGPLAYARAFLDDTNTKR
HC2F	-----

HC2A	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2A-80	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2B	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2C	-----
HC2D	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2E	YPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQ
HC2F	-----

HC2A	ICPLEEKTSVLPNSLHIFNAISGTPSTMVHGMTSSSSVVZ----
HC2A-80	ICPLEEKTSVLPNSLHIFNAISGTPSTMVHGMTSSSSVVZ----
HC2B	ICPLEEKTSVLPNSLHIFNAISGTPSTMVHGMTSSSSVVZ----
HC2C	-----
HC2D	LG-----
HC2E	ICPLEEKTSVLPNSLHIFNAISGTPSTMVHGMTSSSSVVZ----
HC2F	-----

FIG. 3B(cont.)

PBL

lung

placenta

sm intestine

liver

kidney

spleen

thymus

colon

skel muscle

heart

brain

FIG. 4A

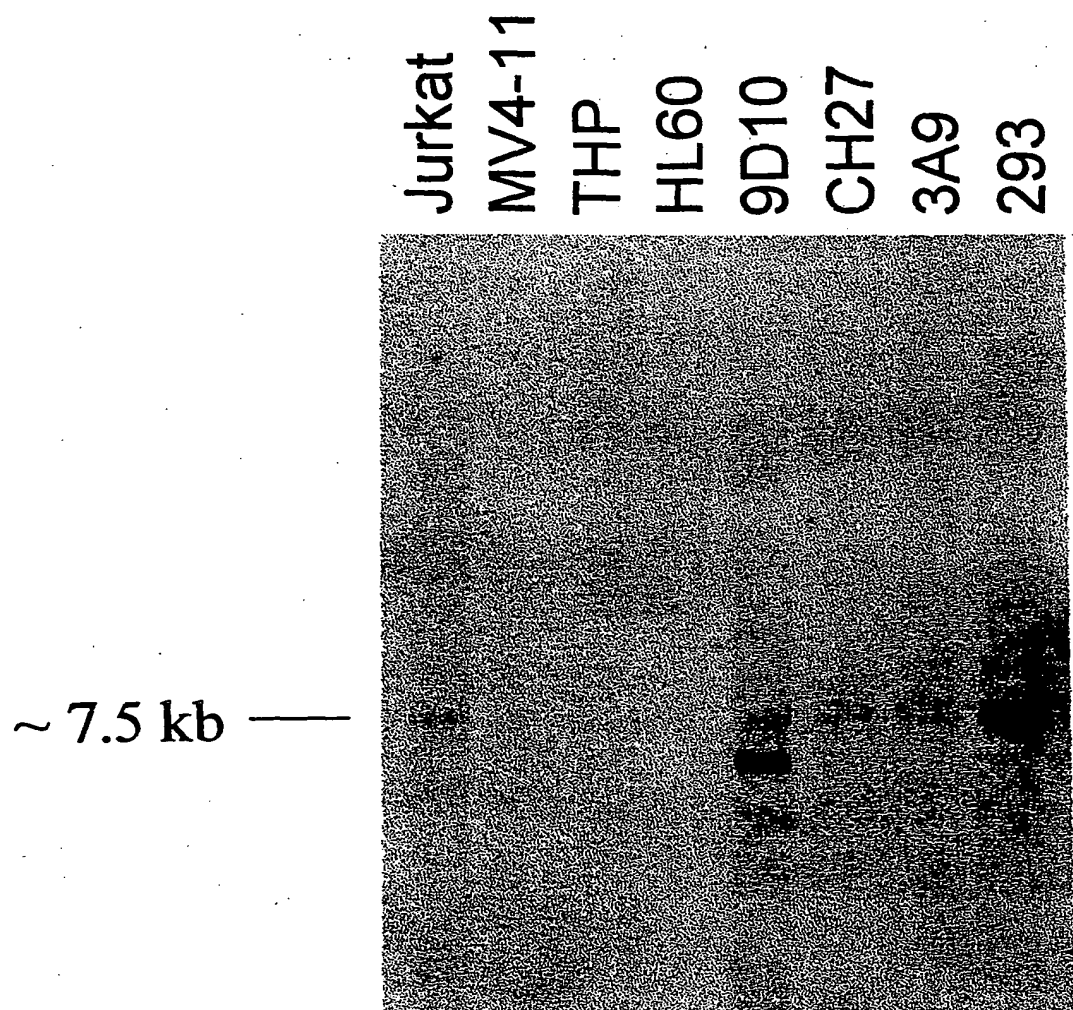


Fig. 4B

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSFARNAIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDOHLHNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDOHLHNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----

HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

FIG. 5A

HC2A	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	IIHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP---TKKLFHEELALQWVVCSSG---SVR---E
HC5	-----

Cadherin

Cleavage

HC2A	KLLRYSWFFFFDVLIKSMAQHLENSKVKLLRNQRFPPASYHHAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFFDVLIKSMAQHLENSKVKLLRNQRFPPASYHHAETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFFAIILKSMAQHLIDTNKIQLPRPQRFPPESYQNELDNLMVVLSDHVIWKYKD
HC3	SALQQAWFFFEELMVKSMVHHLYFNDKLEAPRKSRRFPERFMDDIAALVSTIASDIVSRFQK
HC5	-----

HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSLASFLKCCLTLMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDL
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----

HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVCOHEHFIPCLPIRSANIPDPLTPSES-----TQELHASIMPEYSVTNEF
HC3	RIICSHEHYVTNLNPLCSLLTPPASPSPVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFQDQKIASMFDRTSRVPA

HC2A	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGLLLREVGTALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGLLLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNOQAKIAQ
HC1	CRKHFLIGILLREVGFALQEDQD----VRHLALAVLKNLMKHSFDDRYREPRKQAQIAS
HC3	RQQHYLAGLVLTAVILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGLLFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCPEVKVKIAA

HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPLFVGLLLENIQRLAGRDTLYSCAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

HC2A	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLPERNSEKSNSLDKHQOSS
KIAA	KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNLPERNSEKSNSLDKHQOSS
rat	-----
HC4	TDKDTAYGSFQNG-----HGIKREDSRGSLIP-EGATGFDPQNTGEN-----TRQS
HC1	KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
HC3	QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGROHT-----
HC5	QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

Fig. 5A (cont.)

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL
 HC1 ALIGSTLRFDRLDQAETRSLLMCFHIMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
 HC3 -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV
 HC5 -----MLNADTTNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFOYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
 KIAA HQFOYMGKRYIAR-----TGM
 rat -----
 HC4 FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALRNRSQVM
 HC1 QNFRYLGRNIIRKIAAAF--KFVQSTQNNGTGKSNPSCQTSGLLAQWMHSTSRHEGK
 HC3 SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
 HC5 LCFEYKGGQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEGARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTEADIFHQALLEGNTATEVS
 HC1 QHRSQTLPIIRGK--NALSNPKL----LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
 KIAA LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY
 rat -----KLSRGHSPMLKKVFDVYLCFLQKHQSEMAKNVFTALRSLIY
 HC4 LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
 HC1 LTILDVLSLFTQTHORQLQCCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC
 HC3 LIILDLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAYVLOHCFATQALVS
 HC5 LIILDMQENIIQASS--ALDC--KDSLGGVLRVLVNSLNCQSTTYLTHCFATLALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH
 HC4 KFPSAFFKGRVNMCAAFCEYVLKCCCTSKISSTRNEASALLYLLMRNFEYTKRKTFLRTH
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
 HC3 KFPPELLFEEETEQCADLCRLRLRHCCSSSIGTIRSHPSASLYLLMRQNFIGN--NFARVK
 HC5 KFGDLLFEEVEEQCFDLCHQVLHHCSSMDVTRSQACATLYLLMRFSFGATS--NFARVK

HC2A LQVIISVSQLIADVVGIGETRFOQSLSIINNCANSDRLIKHTSFSSDVKDLTRIRTVLM
 KIAA LQVIISVSQLIADVVGIGETRFOQSLSIINNCANSDRLIKHTSFSSDVKDLTRIRTVLM
 rat LQVIISLSQLIADVVGIGETRFOQSLSIINNCANSDRLIKHTSFSSDVKDLTRIRTVLM
 HC4 LQIIIAVSQLIADVALSGGSRFQESLFIINNFANSRPLARAFPAEVKDLTRIRTVLM
 HC1 LQLIKAVSQLIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFPAEVKDLTRIRTVLM
 HC3 MOVFMSLSSLVGTSONFNEEFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMILS
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLSILY

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGDLSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHVKNGDLSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLDSMAKIHARNGDLSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSDDLRLTLWLQNMAGKHSERSNHAEEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQASDDLRLTLWLQNMAEKHTKKKCYTEAAMCLVHA

SH3

HC2A	TALVAEYI	TRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYI	TRKEA-----	VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYI	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEFI	HRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYI	KRKGWYKVEKICTASLLSEDPHPCDSNSLLTPSGGSMFSGMWPAFLSITPN		
HC3	AALVAEYI	SMLED-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYI	SMLED-----		HSYLPVGSVSFQNISSN

HC2A	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLELLEQCVNGLWKAERYEIISEISKLGPI
HC1	IKKEGAAKEDSGMHD-----	TPYENILVEQLYMCGEFLWKSEYELIADVNKPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASFMSMAGMYEAVNEVYKVLPI	
HC5	VLEESVVSSEDTLSPDEEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPI	

		ITAM	ITAM		ITAM		ITAM
HC2A	YEKRRD-----						
KIAA	YEKRRDFFERLAHIYDTLHRAYSKVTEVMHSGRLLGTYFRVAFFGQAAQYQFTDSETDVE						
rat	SMKSGGTLETTHLYDTLHRAYSKVTEVITR-----				A-----		AGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTLHGAYTKILEVMHTKKRLLG-----						TFFRVAFYFGQ
HC1	FEKQDFKKLSDIYYDIHRSYLKVAEVNSEKRLFG-----						RYRVAFYFGQ
HC3	HEANRDAKKLSTIHGKLOEAFSKIIVHQSTGWERMFG-----						TYFRVGFYFG-
HC5	LEAHREFRKLTLTHSKLQRAFDSDIVNKDH--KRMFG-----						TYFRVGFFFG-

		ITAM		ITAM	
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA				
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA				
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA				
HC4	SFFEEEDGKEYIYKEPKLTGLSEISRLVKLYGKFGTENVKIIQSDKVNKELDPKYA				
HC1	GFFEEEDGKEYIYKEPKLTGLSEISQRLKLYADKFGADNVKIIQSDKNVNPKDLDPKYA				
HC3	TKFGDLDEQEFVYKEFAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPFVDKCKLDPNKA				
HC5	SKFGDLDEQEFVYKEFAITKLPEISHRLEAFYGOQFGAEFVEVIKDSNPFVDKCKLDPNKA				

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVVKPYFDDKELTERKTEFERNHNSRFVFEAPYTLGKKGQCIIEQCKRRTILTT
HC1	YIQVTVVTPFFEEKEIEDRKTDFFEMHNNINRFVFETPFTLGGKKGHGGVAEQCKRRTILTT
HC3	YIQITFYVEPYFDITYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFQRKTILTT
HC5	YIQITFYVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

HC2A	IHCFPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLOLKLQGSV
KIAA	IHCFPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELRQLCSSAEVDMIKLOLKLQGSV
rat	IHCFPYVKKRIPVMYQHHTDINPIEVAIDEMSKKVAELHQLCSSAEVDMIKLOLKLQGSV
HC4	SNSFPYVKKRIPINCEQQINDKPIDGATDEIKDKTAELOKLCSSTDVDMDIQLOLKLQGSV
HC1	SHLFPYVKKRIQVISQSSTEINPIEVAIDEMSRKVSSELNLQCTMEEVDMLQOLKLQGSV
HC3	SHAFPIYKTRVNVNTHKEEIIITPIEVAIEDMKKQTQELAFATHQDPADPKMLQMLVQGSV
HC5	MHAFPIYKTRISVIQKEEFVITPIEVAIEDMKKKTQLQAVAINQEPDPAKMLQMLVQGSV

HC2A	SVQVNAGPLAYARAF	LDDTNTKRY	PDNKVKLLKEV	FRQFVEACGQAI	AVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAF	LDDTNTKRY	PDNKVKLLKEV	FRQFVEACGQAI	AVNERLIKEDQLE
rat	SVQVNAGPLAYARAF	LDDTNTKRY	PDNKVKLLKEV	FRQFVEACGQAI	AVNERLIKEDQLE
HC4	SVQVNAGPLAYARAF	LND	SQASKYPPKKVSEL	KDMFRKFIQACSIAI	ELNERLIKEDQVE
HC1	SVKVNAGPMAYARAF	LEETNAKKY	PDNQVKLLKEI	FRQFADACGQAI	DVNERLIKEDQLE
HC3	GTTVNQGP	LEVAQVFLSEI	PSDPKLFRRHNNKLR	LCFKDFTKRCEDAI	RKNKSLIGPVQKE
HC5	GATVNQGP	LEVAQVFLAEI	PADPKLYRRHNNKLR	LCFKEFIMRCGEAVE	EKNKRLITADQRE

HC2A	YQEE	MKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
KIAA	YQEE	MKANYREMAKELSEIMHE	QLG-----
rat	YQEE	MKANYREIRKELSDIIVE	RICPGEDKRATKFPAPHLQRHQDRTNKHSGSRVDQFILS
HC4	YHEGLKS	NFRDMVKELSDI IHE	QILQEDTMHSPWMSNTLHVFC AISGTSSDRGYGS PRYA
HC1	YQEELRSHYKDMLSELSTVMNE		QITGRDDL SK---RGVDQTCTRVISKATPALPTVS ISS
HC3	YQREL G---	KLSS	PZ
HC5	YQQELKKYNYNKLKENLRPMIER	KIPELYKPI FRVESQKRDSFHRSSFRCKETQLSQGSZ-	

HC2A	<u>SSVVZ</u>
KIAA	
rat	CVTLPEPHVGTCTFVMCKLRITTFRANHWFCAQEEAMGNGREKEPWTVI FNSRFYRSWKG
HC4	<u>EVZ</u>
HC1	<u>SAEVZ</u>
HC3	
HC5	

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----

	A	B	
CLASP-1	YRVAFYGQ:::GFFEEEGKEYIYKEP		
KIAA1058	FRVAFFGQAAQYQFTDSETDVEGFFEDGKEYIYKEP		
CLASP-2		FEDEDGKEYIYKEP	
CLASP-6	FRVAFFGQ:::GFFEEEDGKEYIYKEP		
CLASP-4	FRVAFYGQ:::SFFEEEDGKEYIYKEP		
DOCK180	FAVGYYGQ:::GFPTFLRGKVFIYRGKEYERRED		
DOCK2	FAVGYYGQ:::GFPSFLRNKVFIYRGKEYERRED		
DOCK3	FRVGFYGR:::KFPFFLRNKEYVCRGH		
KIAA0716	FRVGFYGR:::KFPFFLRNKEYVCRGH		
CLASP-3	FRVGFYGT:::KFGDLDEQEFVYKEP		
CONSENSUS	F V FYG YF	KEY K Q F R	
			C
TRG	PKLTPLSEISORLLKLYSDKFGSENVKMIODSGKVNPKDLDSEKFA	XIOVTHVTPPFDEKE	
CLASP-1	PKLTGLSEISORLLKLYADKFGADNVKIIQDSNKVNPKDLPKYAX	IQVTVTPPFEEKE	
CLASP-2	PKLTPLSEISORLLKLYSDKFGSENVKMTQDSGKVNPKDLDSEKFA	XIOVTHVIPPFDEKE	
CLASP-4	PKLTGLSEISORLLKLYGKFGTENVKIIQDSKVNKAKELDPKYAX	HIQVTVKPYFDKE	
CLASP-3	PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAX	IQITYVEPYFDTYE	
KIAA0716	HDYERLEAFQQRMLNEFPFAIA-----MQHANQPDETIFQAEAQ	YLQIYAVTPIPEEQE	
DOCK3	HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDAILQCDAAQ	YLQIYAVTPIPDVVD	
DOCK2	FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGO	YIQCFTVQPVLDHP	
DOCK180	EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPGO	YIQCFTVQPVLDHP	
CONSENSUS	L L Y M F	YIQ+ V P D L E	
	D	E	
CLASP-1	RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN		
TRG	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH		
KIAA1058	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-2	RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR		
CLASP-6	RTILTAIHCFPYVKKRIPFMYQHHTDLNPIEV:HDEMSSKKVAELR		
CLASP-4	RTILTTSNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO		
CLASP-3	KTILTTSHAFPIYIKTRVNVTHKEEIIITPIEVAIEDMQKKTQELA		
CLASP-5	NTVLTTMHAFPIYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLA		
KIAA0716	RTSLYLVSPLPGISRWFVEVEKREVVEMSPLENAIEVLENKNQQLK		
DOCK2	RTSFVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL		
DOCK3	RTTLTLTHSLPGISRWFVEVERRELVEVSPLENAIQVVENKNQQLR		
DOCK180	RTSFVTAYKLPGLRWFEVVHMSQTTISPLENAIETMSTANEKIL		
CONSENSUS	RT L FP V + V + P+E AI+ M +L F L L + I		

CLASP/DOCK MOTIF

DOCK2=KIAA0209
DOCK3=KIAA0299
CLASP2variant=KIAA1058

FIG. 5B (cont.)

2 32
GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT GAG ATT AAA ATA GAG TTG CCC ACT
val leu his his his gln asn pro glu phe tyr asp glu ile lys ile glu leu pro thr

62 92
CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC TTC CAT GTC AGC TGT GAC AAC TCA
gln leu his glu lys his his leu leu leu thr phe phe his val ser cys asp asn ser

122 152
AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA ACC CAA GTT GGC TAC TCC TGG CTT
ser lys gly ser thr lys lys arg asp val val glu thr gln val gly tyr ser trp leu

182 212
CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG CAG CAC ATC CCG GTC TCG GCG AAC
pro leu leu lys asp gly arg val val thr ser glu gln his ile pro val ser ala asn

242 272
CTT CCT TCG GGC TAT CTT GGC TAC CAA GAG CTT GGG ATG GGC AGG CAT TAT GGT CCG GAA
leu pro ser gly tyr leu gly tyr gln glu leu gly met gly arg his tyr gly pro glu

302 332
ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA ATT TCC ACT CAT CTG GTT TCT ACA
ile lys trp val asp gly gly lys pro leu leu lys ile ser thr his leu val ser thr
ref 1.1, 1.2 and 1.3

362 392
GTG TAT ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC CAG TAC TGT CAG AAA ACC GAA TCT
val tyr thr gln asp gln his leu his asn phe phe gln tyr cys gln lys thr glu ser

422 452
GGA GCC CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC CTT AAG AGT CTG CAT GCG ATG GAA
gly ala gln ala leu gly asn glu leu val lys tyr leu lys ser leu his ala met glu

482 512
GGC CAC GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA AAC CAG CTG TTC CGA GTC CTC ACC
gly his val met ile ala phe leu pro thr ile leu asn gln leu phe arg val leu thr

542 572
AGA GCC ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT CGG GTC ATT ATT CAT GTG GTT GCC
arg ala thr gln glu glu val ala val asn val thr arg val ile ile his val val ala

602 632
CAG TGC CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG TCA TAT GTT AAG TAC GCG TAT AAG
gln cys his glu glu gly leu glu ser his leu arg ser tyr val lys tyr ala tyr lys

662 692
GCT GAG CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG CAT GAA GAA CTG ACC AAA TCC ATG
ala glu pro tyr val ala ser glu tyr lys thr val his glu glu leu thr lys ser met

FIG. 4A

722 752
ACC ACG ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC AGC AAC AAA CTA CTG AGG TAC TCA
thr thr ile leu lys pro ser ala asp phe leu thr ser asn lys leu leu arg tyr ser

782 812
TGG TTT TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT CAG CAT TTG ATA GAG AAC TCC AAA
trp phe phe phe asp val leu ile lys ser met ala gln his leu ile glu asn ser lys

842 |Cadherin Cleavage| 872
GTT AAG TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC TAT CAT CAT GCA GCG GAA ACC GTT
val lys leu leu arg asn gln arg phe pro ala ser tyr his his ala ala glu thr val

902 932
GTA AAT ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT GGA GAT AAT CCA GAG GCA TCT AAG
val asn met leu met pro his ile thr gln lys phe gly asp asn pro glu ala ser lys

962 992
AAC GCG AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA TGT TTC ACC TTC ATG GAC AGG GGC
asn ala asn his ser leu ala val phe ile lys arg cys phe thr phe met asp arg gly
ref 2.1 ↓

1022 1052
TTT GTC TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT TTT GCT CCT GGA GAC CCA AAG ACC
phe val phe lys gln ile asn asn tyr ile ser cys phe ala pro gly asp pro lys thr

1082 1112
CTC TTT GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG TGC AAC CAT GAA CAT TAT ATT CCG
leu phe glu tyr lys phe glu phe leu arg val val cys asn his glu his tyr ile pro

1142 1172
TTG AAC TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT CAA AGA TAC CAA GAC CTC CAG CTT
leu asn leu pro met pro phe gly lys gly arg ile gln arg tyr gln asp leu gln leu

1202 1232
GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC TTC TTG GTG GGA CTG TTA CTG AGG
asp tyr ser leu thr asp glu phe cys arg asn his phe leu val gly leu leu leu arg

1262 1292
GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC CGT CTG ATC GCC ATC AGT GTG CTC
glu val gly thr ala leu gln glu phe arg glu val arg leu ile ala ile ser val leu
ref 3.1 ↓

1322 1352
AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA TAT GCT TCA AGG AGC CAT CAG GCA
lys asn leu leu ile lys his ser phe asp asp arg tyr ala ser arg ser his gln ala

1382 1412/471
AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG CTG ATT GAA AAC GTC CAG CGG ATC
arg ile ala thr leu tyr leu pro leu phe gly leu leu ile glu asn val gln arg ile

1442 1472
AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG GGC ATG ACC GTG AAG GAT GAA TCC
asn val arg asp val ser pro phe pro val asn ala gly met thr val lys asp glu ser

1502 1532

Flt. 6A (cont.)

CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG CAG AAG GGA AGC ACC CTG GAC AAC
leu ala leu pro ala val asn pro leu val thr pro gln lys gly ser thr leu asp asn

ref 4.1 and 4.2

1562

1592

AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC ATT GCT TCT CCA TAT ACA ACC TCA
ser leu his lys asp leu leu gly ala ile ser gly ile ala ser pro tyr thr thr ser

1622

1652

ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG AGA GGA TCT CTC ATA AGC ACA GAT
thr pro asn ile asn ser val arg asn ala asp ser arg gly ser leu ile ser thr asp

ref 5.1 and 5.2

1682

1712

TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG AGC AAT TCC CTG GAT AAG CAC CAA
ser gly asn ser leu pro glu arg asn ser glu lys ser asn ser leu asp lys his gln

1742

1772

CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT GAT AAA CTT GAC CAG TCT GAG ATT
gln ser ser thr leu gly asn ser val val arg cys asp lys leu asp gln ser glu ile

1802

1832

AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG AGC ATG TCT GAT GAT GCT TTG TTT
lys ser leu leu met cys phe leu tyr ile leu lys ser met ser asp asp ala leu phe

1862

1892

ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG GAT TTT TTT ACA ATA TCT GAA GTC
thr tyr trp asn lys ala ser thr ser glu leu met asp phe phe thr ile ser glu val

ref 6.1

1922

1952

TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA GCC AGG AAC CAG GAG GGG TTG
cys leu his gln phe gln tyr met gly lys arg tyr ile ala arg asn gln glu gly leu

1982

2012

GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG CCT GTT TCC CGT AAC AGA ACA GGA
gly pro ile val his asp arg lys ser gln thr leu pro val ser arg asn arg thr gly

2042

2072

ATG ATG CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT AAC TCT CTC ACT TTT AAC CAC
met met his ala arg leu gln gln leu gly ser leu asp asn ser leu thr phe asn his

2102

2132

AGC TAT GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG TCA TTA CTT GAA GCC AAC ATT GCT
ser tyr gly his ser asp ala asp val leu his gln ser leu leu glu ala asn ile ala

ref 7.1

2162

2192

ACT GAG GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT CTA TTT ACA TTG GCG TTT AAG AAC
thr glu val cys leu thr ala leu asp thr leu ser leu phe thr leu ala phe lys asn

2222

2252

CAG CTC CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG AAA AAA GTT TTT GAT GTC TAC CTG
gln leu leu ala asp his gly his asn pro leu met lys lys val phe asp val tyr leu

2282

2312

Fig. 6A (cont.)

TGT TTT CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA AAA AAT GTC TTC ACT GCC TTA AGG
cys phe leu gln lys his gln ser glu thr ala leu lys asn val phe thr ala leu arg

2342 2372
TCC TTA ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA GGG AGA GCG GAC ATG TGT GCG GCT
ser leu ile tyr lys phe pro ser thr phe tyr glu gly arg ala asp met cys ala ala

2402 2432
CTG TGT TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG CTG AGC TCC ATC AGG ACG GAG GCC
leu cys tyr glu ile leu lys cys cys asn ser lys leu ser ser ile arg thr glu ala

2462 2492
TCC CAG CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT GAT TAC ACT GGA AAG AAG TCC TTT
ser gln leu leu tyr phe leu met arg asn asn phe asp tyr thr gly lys lys ser phe

2522 2552
GTC CGG ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC CAG CTG ATA GCA GAC GTT GTT GGC
val arg thr his leu gln val ile ile ser val ser gln leu ile ala asp val val gly

2582 2612
ATT GGG GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC ATC AAC AAC TGT GCC AAC AGT GAC
ile gly glu thr arg phe gln gln ser leu ser ile ile asn asn cys ala asn ser asp

2642 2672
CGG CTT ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG AAG GAC TTA ACC AAA AGG ATA CGC
arg leu ile lys his thr ser phe ser ser asp val lys asp leu thr lys arg ile arg

2702 2732
ACG GTG CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT GAG AAC GAC CCA GAG ATG CTG GTG
thr val leu met ala thr ala gln met lys glu his glu asn asp pro glu met leu val

2762 2792
GAC CTC CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC ACG CCC GAG CTC AGG AAG ACG TGG
asp leu gln tyr ser leu ala lys ser tyr ala ser thr pro glu leu arg lys thr trp

2822 2852 1xxxxxxxxxxxxxxxx Predicted
CTC GAC AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC GAT CTC TCA GAG GCA GCA ATG TGC
leu asp ser met ala arg ile his val lys asn gly asp leu ser glu ala ala met cys

Transmembrane Domain xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxI
TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC ACA CGG AAA GGC GTG TTT AGA CAA
tyr val his val thr ala leu val ala glu tyr leu thr arg lys gly val phe arg gln

2942 2972
GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC GAC GAG GAG GCC TCC ATG ATG GAA
gly cys thr ala phe arg val ile thr pro asn ile asp glu glu ala ser met met glu
ref 8.1 ↓

3002 3032
GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT GTG CTG ATG GAG CTC CTT GAG CAG
asp val gly met gln asp val his phe asn glu asp val leu met glu leu leu glu gln

3062 3092
TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG CTC ATC GCC GAC ATC TAC AAA CTT
cys ala asp gly leu trp lys ala glu arg tyr glu leu ile ala asp ile tyr lys leu

```

3122                ref 9.1
ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT GAA GAT GAA GAT GGA AAG GAG TAT
ile ile pro ile tyr glu lys arg arg asp phe phe glu asp glu asp gly lys glu tyr

3182                3152
ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA ATT TCT CAG AGA CTC CTT AAA CTG
ile tyr lys glu pro lys leu thr pro leu ser glu ile ser gln arg leu leu lys leu
ref 10.1

3242                3272
TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG ATA CAG GAT TCT GGC AAG GTC AAC
tyr ser asp lys phe gly ser glu asn val lys met ile gln asp ser gly lys val asn

3302                3332
CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG GTG ACT CAC GTC ATC CCC TTC TTT
pro lys asp leu asp ser lys tyr ala tyr ile gln val thr his val ile pro phe phe

3362                3392
GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT GAG AGA TCC CAC AAC ATC CGC CGC
asp glu lys glu leu gln glu arg lys thr glu phe glu arg ser his asn ile arg arg

3422                3452
TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG AGG CAG GGC GGG GTG GAA GAG CAG
phe met phe glu met pro phe thr gln thr gly lys arg gln gly gly val glu glu gln
ref 11.1

3482                3512
TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC TTC CCT TAT GTG AAG AAG CGC ATC
cys lys arg arg thr ile leu thr ala ile his cys phe pro tyr val lys lys arg ile

3542                3572
CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC ATC GAG GTG GCC ATT GAC GAG ATG
pro val met tyr gln his his thr asp leu asn pro ile glu val ala ile asp glu met
Ixxxxxxxx Coiled-coil 1 xxxxxx

3602 xxxxxxxx Coiled coil 1 cont'd xxxx 3632 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC TCG GCC GAG GTG GAC ATG ATC AAA
ser lys lys val ala glu leu arg gln leu cys ser ser ala glu val asp met ile lys
ref 12.1

3662 xxxxxxxxxxxxxxxxxxxxxxxx 1
CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG GTC AAT GCT GGC CCA CTA GCA TAT
leu gln leu lys leu gln gly ser val ser val gln val asn ala gly pro leu ala tyr

3722                3752
GCG CGA GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA TAT CCT GAC AAT AAA GTG AAG CTG
ala arg ala phe leu asp asp thr asn thr lys arg tyr pro asp asn lys val lys leu

3782                3812
CTT AAG GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC GGT CAA GCC TTA GCG GTA AAC GAA
leu lys glu val phe arg gln phe val glu ala cys gly gln ala leu ala val asn glu
Ixxxxxxxxxxxxxxxxxxxxxxxxxxxxx

3842 xxxxxxxx Coiled coil 2 xxxxxxxxxx 3872 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
CGT CTG ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA GAA ATG AAA GCC AAC TAC AGG GAA
arg leu ile lys glu asp gln leu glu tyr gln glu glu met lys ala asn tyr arg glu

```

ATG GCG AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG ATC TGC CCC CTG GAG GAG AAG ACG
met ala lys glu leu ser glu ile met his glu gln ile cys pro leu glu glu lys thr

3962 3992
AGC GTC TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC ATC AGT GGG ACT CCA ACA AGC ACA
ser val leu pro asn ser leu his ile phe asn ala ile ser gly thr pro thr ser thr

4022 1xxxx PBM xxxxx1
ATG GTT CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG TGA TTA CAT CTC ATG GCC CGT GTG
met val his gly met thr ser ser ser ser val val STP

4082 4112
TGG GGA CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC TTT CCA AAG CCA ATC ACT GGG GAG

4142 4172
ACC GAG CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA AAG GAA ATA AAG AAC AAC GTT ATT

4202 4232
TCT TAA CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG CAC ATA TTT TTT TAA ATC TCA CTG

4262 4292
GCA ATA TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG TGT GGT AGA CAC TCT TGA GCT GGA

4322 4352
CTT AGA TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA ATA GAT GGC CTA CAG AAA AAA AAG

4382 4412
GTT CTG GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA CAT TGA TGC CTG GGG GAC CTT TTG

4442 ref 13.1 4472
CCT CGA CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG TAC AGA ACT TAC TAG TTT TGT CTA

4502 4532
GGA GTA TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC TCA TTC AAC AAC ATA GAG CAA GAA

4562 4592
TAG TGA GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG CTA CTG GCT TCA AGT CAG AAC TTT
ref 14.1

4622 4652
GTC ATT AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT ATT ACA TTT CTA CAT TTT TAA TAC

4682 4712
TCA CAT GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA ATT TGT GCT GGT CCA GTA TAT GCA

4742 4772
ATA CAC TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT GCA ATA TGG AGA TGT ATA CAA GTC

4802
TTT ACT

Flt. Lt. (cont.)

BAC sequences of Human CLASP 2

Ref 1.1

Sequence of BAC4 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 356-375.

TTTCTACAGNGTNTACTCAGGTATGTGCTCCTTCAACAAAATTAGCAGTTGCTGCTCTG
TGACAAAGTTTGCACCATTTTGCAGAAGAAAAAATCCTAATGTGTTATATTACTATA
TTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAAGTGAAGTGCTTATATGTA
TTCATATAAATGACTAGTACAAGCATCATTTTGCACAGATTTCCCCTTTCATTGGAGG
ATCTTCTTGATGTTATTTGTACACGATCAATTTTAGTCTTAATAAGATGAGGCTGGGTG
TGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGATCACTTTAG
CCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTACAAAAATAC
NAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAACTNCCTAGGAGGCTAGG
GGTAGGGGGATTGCAAGAGGCTGGGAGGGTCAAAGCCCNAANTGAGCCATTGGTNC
ATGTCACCTGGACCCCAAGCNGGGGNGANCAAGAGCAAAGGACTNNTGTNNTTTAN
AAAAAAAACCGGGCTACCATAACNACCAACCCNCNACCTACCCNACCTTTCCANNTT
AAAANAAGGCTTTGNCTTGCANAGGAAAANCAAAATNNCC

Ref 1.2

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is underlined and represents nucleotides 351-375.

TCTGGTTTCTACAGTGTATACTNAGGTATGTGCTCCTTNAACAAAATTAGCAGTTGCTG
CTCTGTGACAAAGTTTGCACCATTTTGCAGAAGAAAAAATCCTAATGTGTTATATTA
CTATATTTTACTCTATAGATCTTTTTCTAAAGAAAGAAAGTACAAGTGAAGTGCTTAT
ATGTATTCATATAAATGACTAGTACAAGCATCATTTTGCACAGATTTCCCCTTTCATT
GGAGGATCTTCTTGATGTTATTTGTACACGATCAATTTTAGTCTTAATAAGATGAGGC
TGGGTGTGGTGGCTCACACCTGTAATCCTAGCATTTTGGAGGCCAAGGTGGGCAGATC
ACTTTAGCCCAGGGGTTTGAGACCAGCCTGGCCAACATGGCAAAACCTTGTCTCTACA
AAAATACAAAAATTATCCAGGCATGGTGATGTGTGCCTGTAGTCCCAGCTACCTAGGA
GGCTAGGGTAGGGGGATTGCAAGAGGCTNNGAGGTCAAGGCCCGCAGTGAGCCATGG
TCATGTCACTGCACCCCCAGCCAGGGCCGACAGGAGCAAGACTNTTGTNTCAAAAAA
AACAGNAACCAACANCCAACAACAACNACCTTTCNGCAAAANAAGCTTGCTNCA
ANGAAACCAAAATGNCTTCTTNTTTTCCCCCN

Ref 1.3

Sequence of BAC26 using primer HC2AS2, which spans nucleotides 327-346 of the cDNA. Exon sequence is not found within this sequence. This sequence most likely represent intron sequence since this sequence matches the intron sequence found in the previous two BAC sequences.

AGNNNNNCCCNCTACNCCACTTTTAACCTTTTGAAAACACAGTGTTTNTCTCAANTATGC
GCTCCTTCACATATTAGCAGTTGCTGCTCTGTGACATAGTTGCACCATNTNGCAAGAAG
AAAAAATCCTAAGTGTNATATCACTATATNNNTACTCTATAGATCTTNTCTAAAGAAAG
AAAGTCAACTGATGTGCTTATATGTATNCATATAAATGACTAGTACATGCATCATTTTG
CAACAGATNTCTCCTCACATTGGAGGATCTTCTNGANGNATTCGACACGATNANTATTA
GTCTNAATAAGATGANGCTGGTGTGGNGGTACACTGNATCTAGCATNTGGANGCATGT

Fig. 6A (cont.)

GGCAGACACTTANCCNCGGTNGAGACAGCTGTCACTGNCNAACTGTCTCTNTAAANCA
 AANNCTCCGCNGGNGATGGGCTGAGCCAGTCCTAGNNGCTAGNTAGNGATGNNGAGN
 TGTNGCACGNCGAGNGAGCATGNTCTGTACTGACTCATCAGGCGNCNACACGNTCTGT
 TCNAAAACATAACCACACACACTCNCACCTNCGCAAATTTGCTCTNNAAANATGCTTNT
 TTCACACNGNTNCAATCNCCTATATNNTCTTCTATTCTNCNACGTNTNATTANNATCTTN
 CNCTGCANAAACNATNCGNCCACCTNNANNACCTTANGCTTNGTTTCACGCTTATAGCTC
 CCCTACACNTNNCAGCNNTTNCNNGTGAAGGGCCNCCCGAATCTACGANCACTACTC
 TCCGTATATNGCCTCGGTCANCGCCATCTGCTGTNTNCTCNCCTNCGCNNTTNANCNG
 TNCGCTATCTCTNNNCCGGATCCNCCCATATNNTNNCTCTACTTANAGCGTAANNTNT
 NCNCNCACTANTCACAACCTTNTNCNTNNAACTCTATCTNCTCCTCTCTACCACCTCACT
 TACTACCTNTTTCACNCANTCTCCTTCNCTNTCCACTGATCTCCACATAGCTGCTNTACTC
 GCCANTTTATCATATNCACACNCTCTACGCTNNNTNT

Ref 2.1

Sequence of BAC4 using primer HC2S1, which spans nucleotides 1107-1126 of the cDNA. Exon sequence is underlined and represents nucleotides 1079-1097.

CTTGTATTNAAAGAGGGTCTGCAGGAAGAAGTGTGTAGTCATAAATACCTCACTGGAT
 ATTTTATACAGGATTCTAAAAAACCTATTAGCAATAGTATGCTAGAAATAGTCATTAGC
 TTCTTGACCTTCTTAGAACTGCACACTCTATTGCACTGTACAGATTTTCAGGATGGCTGC
 AGGGATTGATTTGAAAACCTAAGGACACATTTCAATAAACAATGTCTTCAATTGATTTTT
 AGGGCTCCTCCTACTTCAATGAAGGACTTCAGGTAGCTTATAATTACAGACACAGGCTC
 AATACAATAAAAAAATTAGTAAGGCAGAGCTTTAAAAAAGGAAAAAGATAA
 TTCTACCAGAGAAAGGCTACATGGTGACTTCTGTTACCAGTAACAACCCCCGCACTACC
 TTTGGGTCTCCAGGAGCAAAACAGCTAATGTAGTTGTTGATCTGCTTGAAGACAAAGC
 CCCTGTCCATGAAGGTGAAACATCTCTGTGGAGGAAAACAAGCAAAAAAGTTATTTCA
 GGTCCAAACATTTTCGGAAATTTGGATTCAAAGCAGGCATTTATTGCTAATAAGTTTATC
 CACTGACATAAAAAACATGCCTTCAACATTGCCAGAGCACCTACTCTATTNTAGTCNCN

Ref 3.1

Sequence of BAC4 using primer C96AS, which spans nucleotides 1443-1452 of the cDNA. Exon sequence is underlined and represents nucleotides 1370-1422.

AATCAGCAGACCAAACAGAGGCAGGTAGAGGGTGGCTATCCTTGCCTGATGGCTCTGA
 AAAGAAGACACACATGGTAAGTTTGACCCAGGATTCTGAGAACCGAACTAAGTTGGTG
 CTGACCATCTCCTTTATTTGGATCCTTCCTATAAAGACAGATATTTGATTTTAGTCCCAA
 AATAGAGCAAAATCTTAGTGCTGTTACCATGAATTTTCTAACTGATTACTTTCTTTACAC
 CACTTAAAATAAAGGACATTATCAATGCACATTCCTTCCATTGGGGACCACTCACCTT
 GAAGCATATCTGTCATCAAAAGAATGCTTTATCAGCAGGTTCTTGAGCACACTGATGGC
 GATCAGACGGACCTCCCGGAACCTCCTGGAGGGCTGTCCCCACCTCCCTNAGTAACAGT
 CCCACCAAGAAGTGGTTTCTGCAGAACTCATCTGTTAATGAGTAGTCAAGCTGGGAGG
 TCTGAAATGAGGATAGAACTACTTTGNGTTAGGAAAGATGCAATGCTCTTTTGAATA
 AAACAAACAAACCAAAACNAACAAAAAATAAGACCCATCCTTNTGNATTTCAA
 GCCCACCCTGGGGTNGGTCAAAGAGATGATCAGNANTTTGGCNTTNAAATGAAGAAAG
 AAATNAATTNTCCAGGGGNTGTTCTNCTTTTATGCACANGGAGGGATNTTAANTGAAA
 ACCAATTTAAATCCAATTNAGGNG

Ref 4.1

Fig. 6A (cont.)

Sequence of BAC4 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCTTTCTGCAAGGCTGTTCCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGCA
TTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAATC
AAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTTTA
AGGGAAATTGCTTTTATTGCACTTATTTTTCTGTAGGAAGTTGGCTCAAGAGTTGCAT
TCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAGAACTAGT
CTGAAACATTGAGATGTAAACATCAATTCACCTTGTAGAAACCACCTTTGATCGCTAAA
GACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATTAAG
ATAAATCCACCTACAACCTATCAAATCACAAAATTAACCACACAACAACTTGTAGCA
TTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACTCTGAGGGGTGTCATGGGGTA
TTTTAAATTTTCGAGGAGAACACAGTGATATGTGACCTCAGCCAGAAGCTGCTGTTTNA
GCAGCAGGTTGGTGCTATGCTCCTTTTTGAAGACATTTTGTGAAGCTGGGTATTTTG
GGGGCCTGCTTATGATAAAANGGCAAGGTNTTCAATGNAGGGGN

Ref 4.2

Sequence of BAC26 using primer C2AS5, which spans nucleotides 1716-1735 of the cDNA. Exon sequence is underlined and represents nucleotides 1602-1703.

TTCTTTCTGGAAGGCTGTTACCCGAATCTGTGCTTATGAGAGATCCTCTCGAATCAGC
ATTTCTCACACTGTTGATGTTTGGAGTTGAGGTTGTATATGGAGAAGCTAAATGGAAAT
CAAGCCAACAATAAAGTTTTATTAAGACAGAACAAAATAAAGATGAGTACTGAACTTT
AAGGGAAATTGCTTTTATTGCACTTATTTTTCTGTAGGAAGTTGGCTCAAGAGTTGC
ATTCCATTACTTCACCTTTAAAGAACCAGGTCATATACAATGAGATAAAAAGAACTA
GTCTGAAACATTGAGATGTAAACATCAATTCACCTTGTAGAAACCACCTTTGATCGCTA
AAGACTAAATGCATACCTGTTTCAGAATGTGATAGAATGAAGACTTAAAAAAATTA
AGATAAATCCACCTACAACCTATCAAATCACAAAATTAACCNCAACAACAACTTGTAG
CATTCAAACCTGGTAATAAAACACTGAGGAGCCTACCCAACTTTGAGGGGTGTCAATGG
GGTNTTTTTAAATTTTTCGNGGGANANCCAGTGNTATGGTGACCTTCACCCAAGAAGC
TTGTTTGTNTNACCAAGCNAAGGTTGNNCTNTGCTCCTTTTTAGAAANACNNTATTTTNN
AAATNCTGGNTTTTTTNNNGNGGCCCTNCNTTNT

Ref 5.1

Sequence of BAC4 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1724-1736.

TTCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTATAATCAATGGATTT
AGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGTGACCTTTTGTTTTTT
CTAAACCACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGGTTGGGGCCCATTC
CTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTGGGCAGGGTTTGCAGTGG
AGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACTCAAAATGCTGCCC
ATCTCAATTTCTGTAGTCTTTTTATTTATTTATTTATTTTTTGAGACAGAGTCTCGCTCT
GTCGCCCAGGCTGGAGTACAGCGGCACGATCTCAATTNACTGCAACCTCCGCCTCC:TG
GGTTCAAACGACTCCTCTGCCTCAGCCTCCCCAGCAGC:TGGGACCACAGGCACAAGCC
ACCACCGCCCGGCTAATTTTTTGTNTTTTTAGTA:GAGAT:GGGGTTTCACCATATTTGGC
CAGGCTGGGCTCAAACCTCTGACC:TCGTCATCCGCNCCCTCGGNCTNCCAAAGTGCTT
GGGATTNCAGGCNGTGAGCCCACTTACACCTNNGGCAATTCCTGTNAGTCTTTTTTAC
CAGAGACACCATCATTCAACACAGCTTTTCCACCCACAA

Fig. 6A (cont.)

Ref 5.2

Sequence of BAC26 using primer C2S6, which spans nucleotides 1686-1705 of the cDNA. Exon sequence is underlined and represents nucleotides 1712-1736.

TGAGAAGAGCAATTTCTGGATAAGGTAATTGCTTTTACCCAACACAAATGTTTCTTAT
AATCAATGGATTTAGCCCAAAGTAAACGTACTTCATGTTCTAGTGCCTTTTAAGTGTGA
CCTTTTGTTTTTTTCTAAACCAACCCGGCTGACCTGGAGTAGGTGATGAGAGCTTTAAGG
TTGGGGGCCCATTCCTTGAAGTGCTCTGATTCCTGTTTCCAGTACCTCAGATCCTGGGCA
GGGTTTGCAGTGGAGCGTCTTGAGTGAATGGCTCTGGTGGGTTGAACGGGGAGGGACT
CAAAATGCTGCCCCATCTCAATTTCTGTAGTCTTTTTATTTATTTATTTATTTTGGAGAC
AGAGTCTCGCTCTGTGCGCCAGGCTGGAGTACAGCGGCACGATCTCAATTCAGTCAA
CCTCCGNCTCCCTGGGTTCAAACGACTCCTCTGNCTNAGNCTCCC:AGCAGCCTGGGAA
CCACAGGCTCANGCCACCACGCCCCGGCTAATTNTTGAATTTTNAGTAANAAATTGGG
GGTTCTACCATNTTGGCCCAAGNCTTGGGCCTAAAAACCTTNCTNACCNTCGNCATTC
NCNCCCNACCNTGGGCNCTNCTCAAANGNGCTTGGGGATTANCANNGGCNTTAACC
CCCCNTATCACCGTGGNCCTTAATTT

Ref 6.1

Sequence of BAC4 using primer C2S7, which spans nucleotides 1918-1937 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S7 is intron sequence.

NAGNGNGGGTTTNAGNCGTTTGAAGCCTGNNACGNGGTGNGTGCTNGAACTCTGTGGG
CTTTCAGGTAAGTGGGATCTGGGAGCCTGCTGTTTGCATTGCTAGTGCATCAGACCAG
GGCTTTTTCTCCCTGTAGCTGCTACTTATACACATAGCTCTAACTGAGATGATTCTCCA
GACAACTGATGCAGAGCAGCAAAAGCTTCTGCCGTTCTCCCTTCTAGGAGTGTCTCCT
TTCTTTGGAAAGAGATCATGAGGGGCTAGATTGTAATGAAGTGAGGCTCAGTGCTTGA
GCACATCCGGTAAAAGTTCCAATATATTGGTCATAAAGTTTCTCATTCTTTATAGCAGT
TAATTTCTCTGGCTCATGAGTTTTCTTAGTTTTAATCTGACTTTTAAATTAATGTCTCCA
GCACCAGTCATATCCCCAGGGCAAACCTCAAAGGCATGAGAGGCCAGACTCGGGTCCCTG
GTCATAGCAACCCCTGTCTAGGGCCTTGGTCCCTGCCTCCGCTTGTGTGCTGTGGCGCA
GGTCCATAGGGCCCTTAGGAAACAGGACCACCCTGTGCGACCCCTACAGAGACCAGC
CAAGTTTGACATTAGATCACCGTAGCAATGTNTGCAAATTCCAGTTTCTTGCTAAAACA
GGTTAAGCCTTGCAGCCACTTTATCTGTAAGTGGCNGAGGTTTTGACATAAAA

Ref 7.1

Sequence of BAC4 using primer C2S8, which spans nucleotides 2143-2162 of the cDNA. Exon sequence is underlined and represents nucleotides 2182-2219.

CTCTCGACACGCTGTTTCTATTAACATTGGCGTTTAAGGTTTGTATCAATTTGCTGTTCTG
NGGTTCTAGTTTTACCTTTCACATTCATTCTGCTTGGTAAGCTCAGTGAGCACAAACTTA
CTATGTTGCATTTTTACTTCAGCAATTATTTTTGTCCCTGTAAGGAAACCATTAATCTTT
AAATTCCTTTAATGAAATCATTCCACAGTGAATGGCTTGAATGCCCTGAAATAAAATTT
AACTGGTCAGTGTGTGCTGCGCGCTTGGGTATGGTGGAAACACGGTCTCTGGAGGCAG
TTAACTCTTGGCTCGAACCTTGAGGATGGTGAATATAGGCACCTAATCAGGCATTTCTG
CCTTGAATATCTTTAAATATATCCAAATGTTATAGCGTTTAATTAGATTTTTATGTAGAA
AGGAGCAATAAACACAAGACACATGTTTTTCAAGTTTTTATCTGTTACTGCATTAAATGA

Fig. 6A (cont.)

TAAAAACGTTTTGGAGATAGAAAATGAAAGGGGTTTTTTTTTTGTCTTGTTTTAAAGTT
TTAGCAAATAATATTCAAGTAGGTGGAGATGGACTCTTCACCACTCTCCTGTTTTTAGG
AACCCAATACTTTTTATTCTTGCTAAATGATTACTTCCATTCTAGCATAGAAAAGGA
GAAAATTGGAATGAGTGTTTATAT

Ref 8.1

Sequence of BAC4 using primer C2S9, which spans nucleotides 2992-3011 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

CGCTTTNAAATNCCAGCCGCTACTGCGGGGCGNTNAATTTCGAAACGTGTTGTTNTCTGT
GATGCCTGGCTCTGATTGTGTGGGATTGGTCATCAGTGGCGGTTGGCAGNTGGGGTTCA
TGGAAGCGGCCATGGGGACTGATGGCAGGCCCTTGGATTGCCACCGCAGAGCCTGGCA
GTGTCTTTGGTCTGCATTCCCTACCGGCGAAGTCTCATTTACCTCACGTGTTATCTCTTG
GAAAGCATTCCCTTAGCGGGCTGTGTCTACCTTCCATCCTCTCGTCCAAACTCCCCCTC
CTTCTCTGTTCTGTCTCCTTCCCATCCTCTTCTCCCCAGTTCTTCTTCTCCTATGTTCCCTCCT
CAGTGGTTTCTCTTCTCTGTTTGAAGTCTTCAAGGTCATTTTGAAGTCTTCTGCTCCCAA
CTACAAAGATACTAAAATCTCACCTAACCACTCTTCTTCTTCTTAATGAAAGAATGTT
TTCAGTCCATCCCAAATTTGTGTGGACTTCACAAACCTTCTCTAAAATGGAGCCTTTTCT
CTTCTACTCTTGACTAGNTGGTAAACGCTCCATGTTCTTGGCCAGAAGTCCCTGGTGA
GTAGCGTCACTCCCACTTTCTGTGCAGAACCAAGCCTCCTAGAAAAGTCTTTTGCANC
TGAGTGGGTTGGGACACGCCCTTTNTTTGGG

Ref 9.1

Sequence of BAC4 using primer C2AS10, which spans nucleotides 3276-3295 of the cDNA. Exon sequence is underlined and represents nucleotides 3147-3234.

TTTANACCNATNTATCCGNGTCAGTTANAGGAGTCTCTGAGAAATTTCCGACAGCGGT
GTGAGTTTGGGTTCCCTGTAAATATACTCCTTTCCATCTTCATCTTCAAAGAATCCCTGT
GACATAAAGCACAATTAGAGCTATCCCTGAACGTAAGCCCAGGGCTTACCACCTAGGA
AGCGTTCTTTTATTACAAGGGGGGAAAAAAAGGAATGGGTCTAAAAATCCAGCTGAAAT
GGGCTTTCTGAATGAGAAAGAAAAATGCTAATAACATGAAGTCTAGGTGCAAAGGTAAA
GGAAAAACACAACATTGCAAACCTTATTCAAGAATGCAGTCATTAAGTGTGAGTGAAA
TGAAAGATTTTGGATACAAGACTAAGCTGTCCCAGGGGAAGTCTAATGGGAGTCAAGCC
TGTTTCACTTTCCCAAGAAGCAGAACTCACTANAAAAATGATGAGCAGCCCACGACAGG
CAGGCTCAGAAGTGGACATGCCTCCCTTCTCCTGATGGCTNCCATGCACACAGGATTTT
ATGGCATGAACTGAAGCGTTTGGGGGTCTGGAGTAAGTTTAGTAAAAGTTAGGTAAAG
CTTGATAAATTGTATTTTGTCTTACCCGATGAGAAAAAAATATTNAAGACCTGGTA
GCTTCAATATTCAAGAAAAATATTTTTCATNTCACCCG

Ref 10.1

Sequence of BAC4 using primer C2S11, which spans nucleotides 3167-3186 of the cDNA. Exon sequence is underlined and represents nucleotides 3231-3296.

NGNANGTGGAGCCNCGANCCAGGGACAATCTNAACCTNCTTAAACTGTACTCGGATNA
ATTTGGTTCTGAAAATGTCAAAATGATACAGGATTCTGGCAAGGTATTGACCATGTTTG
GANAAGTTTTCATAGCAATGTAATGTTGTGATNCGATTACATATNATATATTTTAAATG
TNTATAGAAAAAAACACANGAAAAATATTAAGGATTGTTGGCCCGTGAGTGGCAGGTG
TATNTTCTTNCTGATCCTTTAGNGCTTCCATTACATGCNTGACATTAAAAAAANCTTTA

Fig. 6A (cont.)

TCGCCTAATTTTTGAAACATCTAATTTTACAAAATAATTAACCGTNTGGCCANGNATAT
 TNTCATTTTTAGGNCCAGCTATTTAGAACTCTGACANAAATGAGGGGCTGTGGCTTNC
 CTNCCTNNACTTGNCCTCTTTTCNNGNATGTACCACATGAACTTGNCNCCTCTTTTCNNC
 TNACCGGGTGGCATGTTANAGGACAGGTTGAAACCNCANTNGGGCNGGANTTNGGTN
 NAATTGGGACACAATGGTACNANGCTCTATNGGAATNGAACTCTCCCNACNNNCNGT
 GNNCCNTGGGGAAAATGNGNCNNATTCATTTTN

Ref 11.1

Sequence of BAC4 using primer C2S12, which spans nucleotides 3474-3493 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from C2S9 is intron sequence

AGNANNGTTNNGCAGCTGCANNTCTGGACCCANAGGCCGCANGGGCACGAGCCNGGA
 CACGCTCGGCAAAGAGCTGTCCAGAGGGATTGAGAAGCTTCAGGACTGGAAGGGTCTT
 TCGAGCTCAGTTAGCCACCCCCACACCCATTTTCAAGTTTACATTTATCTAGTGCTTCCTT
 TTGAATACTTGGGATGTTTTTCTGTTGATCTGTTGGCACTTCCTTCTTCCACAAGACCAG
 AAGCTCATATCCAATCTAAGGTCACCTACCCTTCTGAGAATCTGATGAAAATGGCGTGC
 CTTATGTGCCTAGATGCTTTTGCACACAGTCTAAGGTGACTTATGGACTCCAGGTCCAG
 CAGCCACACCCAGTCTGCGGTCTCCGCACAGGGAGGGACCCGCTTTCACACACCTGTCT
 CAGGTTCTAGCATTGGGCTGCTTCAGCGGTCTCAGGCTGTGAGTAAATGGGATGTGAG
 CTTGGATCGCCCCACGCTGTTGNCCCCCGGGGGGCTTGGCCAGCTGGCCACTTNGAAAT
 GCCTCCTTTTGCCAGGAAAGCTCACTGCATTTCAATGGGGNTTNTCCACGAAGTTCAN
 CTTTANGGG

Ref 12.1

Sequence of BAC4 using primer C2S13, which spans nucleotides 3645-3664 of the cDNA. Exon sequence is underlined and represents nucleotides 3683-3699.

AGNAAGGTNNCTCANTNAANNCAGCGTGAGNGTTCAGGTGAGCCAGGCACAGCAGGC
 CGGAGGGCAGCAGGGGACGTCCTTGCCCCCTGGGTGACTTGAGAGTCGTTTCCACTAAC
 AAGGTCTACTTGAGAGCCTCGGTTTACCAAGTGATCCCTGCTCCCTTCCCCCAACGTNT
 GTGACATTTCTCCTGATATCAGAGGGGGAGGAAACCTCATGATCCCTGCCCCCGCCCC
 ATGAGGACTGACTGTGGGGACAAAGAGCCAGATCTCATAGACTACCCTGATTTGTGAG
 TATTTGGGAATTCTGGGTGCCTGATTAGAAGCATCAAGACTCTTCTAAATNCAAAGA
 AGTGTGGAGAGCAGTAGATTTTCCTATAAACTGGTGTGCTGGTTTCTATGAAAATTG
 GATCCAAAAAAGTCCTTAAGTTTACCCTCTTAATGGNATCTTTTGATTAATGGAATTC
 ATTATTTTAATATAGCCCAATCAATCCAATTTTCTTTATTGGTAGCATTTTATGTTCTC
 TTTAAAAAATCTTGGNCTACCTCCAAAATTTACAGATGTTCTCCTAGGGTTTTCTCC
 TTTTGTTCAAGCATCCCATTCAANGTCTTGCAAGTCCATTCTGGGG

Ref 13.1

Sequence of BAC4 using primer C2S14, which spans nucleotides 4289-4308 of the cDNA. Exon sequence is underlined and represents nucleotides 4321-4448.

GACTTANATTTATTCTTCCTTGCAGAGTAGTGTTAGAAATAGATGGCCTACAGAAAAAAA
AGGTTCTGGGATCTACATGGCAGGGAGGGCTGCACTGACATTGATGCCTGGGGGACCT
TTTGCTCGAGGCTGAGCTGGAAAATCTTGAAAATATTTTTTTTCTGTGGCACATTC
 AGGTTGAATACAAGAACTATTTTGTGACTATGTTTTTGATGACCTAAGGGAACTGACC
 ATTGTAATTTTTGTACCANTGAACCANGAGATTTAAGTGCTTTTATATTCAATTCCTTGC

Fig. 6A (cont.)

ATTTAAGAAAATATGAAAGCTTAAGGAATTATGTGAGCTTAAAAGTCAAGCANTT
TAGAACCAAAGGCCTATNTTNATAACCGCAACTATGCTNAAAAGNACAAAGTAGTACA
GNATATTGNTATGTACATATCATTTGGTAATACACNCCNGGCNTTCTGTACATATATGT
ATTACATTTCTACNTTTTTAATACTCCCNTGGGCTTATGCCNTTAAGGTTAANTTGNGAT
AAATTTNGGCTGTTCCNGTNTATNCNATACNCTTTT

Ref 14.1

Sequence of BAC4 using primer C2AS15, which spans nucleotides 4680-4700 of the cDNA. Exon sequence is underlined and represents nucleotides 4660-4683.

ATGAGAATGTAATACATATATGTACAGAATGCCAGGACTGTATTAACAATGATATGTA
CATAACAATATACTGTACTACTTTGTACTTTTCAGCATAGTTGCGGTTATTAATATAGG
CCTTTGGTTCTAAACTGCTTGACTAGTTTTAAGCTCACATAATTCCTTAAGCTTTCATAT
TTTCTTAAATGCAAGGAAATGAATATAAAAGCACTAAATCTCCTGGTTCACTGGTACAA
AAATTACAATGGTCAGTTCCTTAGGTCATCAAAAAGTCAACAAAAATAGTTCTTGT
ATTCAACCTGAATGTGCCACAGGAAAAAAAAAATATTTTCAAGATTTTCCAGCTCAGC
CTCGAGGCAAAAGGCCCCCAGGCATCAATGTCAGNGCAGCCCTCCTGCCATGTAGATC
CCAGAACCTTTTTTTTTCTGTAGGCCATCTATTCTAACACTACTCTGCAGGGAGAATAAA
ATCTAAAGNCCAGCTCAAGAGTGCTACCACACCTTTGTTAAGACACAATGAAAACCTTT
GGATATTGGCAGGNGAGATTTAAAAAAAAAATGTGCCCTTTCTTACCACTCCTATAGNA
AAGTCTGGTTAAGAAATAACCGTTGGTCTTTATTTTCCTTTNTTTCCCCTTCCCTTGGG
NCTTCCTGGGGCTCGG

Fig. 6A (cont.)

HC2A
KIAA ASGNL DKNARFSAIYRQDSNKL SNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat
HC4
HC1
HC3
HC5

HC2A
KIAA FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSO
rat
HC4
HC1
HC3
HC5

HC2A
KIAA -----VLHHHQNPEFYDEIK
rat KSAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
HC4
HC1
HC3
HC5

HC2A
KIAA IELPTQLHEKHHL LLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat IELPTQLHEKHHL LLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
HC4
HC1
HC3
HC5

HC2A
KIAA PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
HC4
HC1
HC3 -----GPGPARSTVSISLISNSARV
HC5

HC2A
KIAA OKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat OKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
HC4 -----MEIQVLIRFLSVILMQLFWLPNMIHEDDVPISCPMV
HC1 -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3 NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5

Fig. 6B (cont.)

HC2A I I H V V A Q C H L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
 rat
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R A C K E R P V H E D L A K N V T G L L K S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P T K K L F H E E L A L Q W V V C S G S V R E
 HC5

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T I V E S Q Y A E
 HC1 H V L K I S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5

6.1
 1.1 / 1.2 / 2.1 / 2.2

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N N Y I S C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N N Y I S C F A P G D P K T L F E Y K F E F L
 rat
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N D Y I S G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N N Y I S M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y Q V S S K L Y S L P N P S V I V S L R L D F L
 HC5

2.1

7.1

3.1 / 3.2

HC2A R V V C N H E H Y I P L N L P M P F G K G R I Q R Y Q D L Q L D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M P F G K G R I Q R Y Q D L Q L D Y S L T D E F
 rat
 HC4 Q T I C N H E H Y I P L N L P M A F A K P K L Q R V Q D S N L E Y S L S D E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D P L T P S E T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L P C S L L T P P A S P S P S V S S A T S Q S S G F S T N V Q D Q I A N M F E L S V P F
 HC5 M N A D T A P T S P C P S I S S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

4.1 / 4.2

HC2A C R N H F L V G L L L R E V G T A L Q E F R E V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E V R L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D Q D V R H L A L A V L K N L M A K H S F D D R Y E R P R Q A Q I A S
 HC3 R Q Q H Y L A G L V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S S P G L L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

3.1

8.1

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat
 HC4 L Y L P F V G L L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F P C G F T S P A N R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E S G S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R T S G S D E E Q E G A G A I T

9.1

4.1 / 4.2

HC2A K D L L G A I S G I A S P Y T T S T P N I N S V R N A D S R G S L I S T D S G N S L P E R N S E K S N S L D K H Q Q S S
 KIAA K D L L G A I S G I A S P Y T T S T P N I N S V R N A D S R G S L I S T D S G N S L P E R N S E K S N S L D K H Q Q S S
 rat
 HC4 T D K D T A Y G S F O N G H G I K R E D S R G S L I P E G A T G F P D Q G N T G E N T R Q S
 HC1 K D V L N S I A F S S I A I S T V N H A D S R A S L A S L D S N P S T N E K S S E K T D N C E K I P R P L
 HC3 Q T V A M A I A G T S V P Q L T R P G S F L L T S T S G R O H T
 HC5 Q N V A L A I A G N N F N L K T S G I V L S S L P Y K Q Y N

5.1 / 5.2

10.1

3.1

2.1

HC2A	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
KIAA	TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL	
rat	-----	
HC4	STRSSVSQYNRLDQYEIRSLLMCYLYIVKMI SEDTLLTYWN-KVSPQELINILILLEVCL	
HC1	ALIGSTLRFDRDLQAETRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIPVCL	11.1 / 11.2
HC3	-----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV	
HC5	-----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV	
HC2A	HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM	6.1
KIAA	HQFQYMGKRYIAR-----TGMM	
rat	-----	
HC4	FHFRYMGKRNIARVHDAWLSKHFGIDRKS-----QTMPALNRNRSGVM	
HC1	QNFRLGLKRNIIIRKIAAAF--KFVQSTQNNGTLGKSNPSCQTSGLLAQWMHSTSRHEGHK	
HC3	SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSI GARQEMV	
HC5	LCFEYKGGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM	
HC2A	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
KIAA	HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC	
rat	-----	
HC4	QARLQHL-----SSLESS-----FTLNHSSTTTEADI FHQALLEGNTATEVS	
HC1	QHRSTLPIIRGK--NALS NPKL----LQMLDNTMTS NSNEIDIVHHVDTEAN IATEGC	12.1 / 12.2
HC3	RRSRGQLERSPSGSAPGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN	6.1 / 6.2
HC5	RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH	
HC2A	LTALDTLSLFTLAFKQQLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIY	7.1
KIAA	LTALDTLSLFTLAFKQQLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIY	
rat	-----KLSRGHSPMLKKVFDVYLCFLQKHQSEMA LKNVFTALRS LIY	
HC4	LTVLDTISFFTQCFKTHFLNNDGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS	
HC1	LTILDVLSLFTQTHORQLQQCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC	13.1
HC3	LIILDLTLEIVVQTVS--VTES--KESILGGVLKVLHLSMACNQSAVYLQHC FATQALVS	
HC5	LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLALIA	3.1
HC2A	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN NFDYTGKKS FVRTH	
KIAA	KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN NFDYTGKKS FVRTH	
rat	KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRN NFDYTGKKS FVRTH	
HC4	KFPSAFFKGRVNMCAAFCEVLKCCCTSKISSRNEASALLYFLMRN NFEYTKRKTFLRTH	
HC1	KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYFLMRK NFEFNKQKSIVRSH	
HC3	KPELLFEEETEQCADLCRLRLRHCCSSSIGTIRSHPSASLYLLMRQ NFEIGN--N FARVK	7.1 / 7.2
HC5	KFGDLLFEEVEQCFDLCHQVLHHCSSSMDVTRSQCATLYLLMRFS FGATS--N FARVK	
HC2A	LQVIISVSQLIADVVGIGETRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
KIAA	LQVIISVSQLIADVVGIGGTRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
rat	LQVIISLSQLIADVVGIGGTRFOQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLM	
HC4	LQIIIAVSQLIADVALSGGSRFQESLFI INNFANSRPM LARAPPAEVKDLTKRIRTVLM	
HC1	LQIIKAVSQLIAD-AGIGGSRFQHS LAITN NFANGDKOMKN SNFPAEVKDLTKRIRTVLM	14.1 / 14.2 / 15.1
HC3	MQVPMSLSSLVGTSONFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMHILS	
HC5	MQVTMSLASLVGRAPDFNEEHLRRSLRTI LAYSEEDTAMQMTFPPTQVEELL CNLNSILY	

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIVKNGDLSEAAACVYHV	16.1 / 16.2
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIVKNGDLSEAAACVYHV	
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIVKNGDLSEAAACVYHV	
HC4	ATAQMKEHEKDPEMLVDLQYSLAKSYASTPELRKRWLDSMAKIVKNGDLSEAAACVYHV	
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAACVYIHI	
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTSPLRLTLWLQNMAGKHSERSNIAEAAQCLVHS	
HC5	DTVKMREFQEDPEMLMDLRYIAKSYQASPLRLTLWLQNAEKHTKKKCYTEAAMCLVHA	

		SH3	
HC2A	TALVAEYITRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYITRKEA-----		VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYITRKEAD-----		LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEYITRKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYITRKGYSKVEKIC-----		TASLLSEDTHPCDNSLLTTPSGGSMFSMGWPAFLSITPN
HC3	AALVAEYITSMLED-----		RKYLEPVGCVTQNISSN
HC5	AALVAEYITSMLED-----		HSYLEPVGSVSFQNISSN

HC2A	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP	9.1
KIAA	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP	
rat	IDEEASMMEDVGMQD-----	VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIIP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEEVLLLELLEQCVNGLWKAERYEIISEISKLGPI	
HC1	IKKEGAARKEDSGMHD-----	TPYNEILVEQLYMCGEFLWKSEYELIADVPKPIIAV	
HC3	VLEESAVSDDVVSPEEGICSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKVLIP		
HC5	VLEESVVSSEDTLSPDEGDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLIP		

		ITAM	ITAM	ITAM	ITAM	
HC2A	YEKRRD-----					
KIAA	YEKRRDFERLAHLDTLHRYYSKVTEVMHSGRRLGTYFRVAFFGQAAQYQFTDSETDVE					
rat	SMKSGGTLETTHLYDTLHRYYSKVTEVITR-----					AGSWDLLPGGLFGQ
HC4	YENRREFENLTQVYRTLHGYTKILEVMHTKKRLG-----					TFERYAFYGO
HC1	FEKQRDFKKLSDLTYDIHRSYLKVAEVDNVEKRLFG-----					RYFRVAFYGO
HC3	HEANRDAKKLSTIHGKLOEFYSKIYHQTGWERMFG-----					TYFRVAFYGO
HC5	LEAHREFRKLTLTHSKLDRAEDSIYNKDH--KRMFG-----					TYFRVAFYGO

HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	10.1
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDKFGSENVKMIQDSGKVNPKDLDSKFA	
HC4	SFFEDEDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSKVNNAKELDPKYA	
HC1	GFFEDEDGKEYIYKEPKLTGLSEISQRLKLYADKFGADNVKIIQDSKVNNAKELDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRIEGFYGERFGEDVVEVIKDSNPNVCKKLDPNKA	10.1 / 10.2
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRIEAFYGOFCGAEFVEVIKDSNPNVCKKLDPNKA	4.1

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA	11.1 / 11.2
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA	
rat	YIQVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA	
HC4	HIQVTVKPYFDDKELTERKTEFERHNISRFVFEAPYTLGKKQGCIEEQCKRRTILT	
HC1	YIQVTVYVTPFFEEKEIEDRKTDFFEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT	
HC3	YIQITYVEPYFDYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGEHQFRRKTILT	18.1
HC5	YIQITFVEPYFDEYEMKDRVITYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT	

Coiled-Coil 1

HC2A IHCFFPYVKKRIPVVMYQHHTDLNHEIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLOGSV
 KIAA IHCFFPYVKKRIPVVMYQHHTDLNHEIEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLOGSV
 rat IHCFFPYVKKRIPVVMYQHHTDLNHEIEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLOGSV
 HC4 SNSFFPYVKKRIPINCEQQINLKEIDGATDEIKDKTAELOKLCSSSTDVDMIQLQLKLOGSV
 HC1 SHLFFPYVKKRIQVISQSSTELNHEIEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLOGSV
 HC3 SHAFPIKTRVNVTHKEIEIILTHEIEVAIEDMQKKTQELAFATHQDPADPKMLQMVLOGSV
 HC5 MHAFPIKTRISVIOKEEFVLTHEIEVAIEDMKKKTLLQAVAINOEPPDAKMLQMVLOGSV

11.1

Coiled-Coil 2

HC2A SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
 KIAA SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
 rat SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
 HC4 SVQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFIQACSIALLNERLIKEDQVE
 HC1 SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
 HC3 GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE
 HC5 GATVNOGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

11.1 / 12.1

Coiled-Coil 2

HC2A YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
 KIAA YQEEMKANYREMAKELSEIMHEQICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
 rat YQEEMKANYREIRKELSDIIVPRICPGEDKRATKFFPAHLQRHQRTDNKHSGSRVDQFELS
 HC4 YHEGLKSNFRDMVKELSDIIEHQILOEDTMHSPWMSNTLHVFCASISGTSDDRGYGPBYA
 HC1 YQEELRSHYKDMSELSTVMNEQITGRDDLK---RGVDQCTRVISKATPALPTVSISS
 HC3 YQRELK---KLSS---PZ---
 HC5 YQRELKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-

19.1

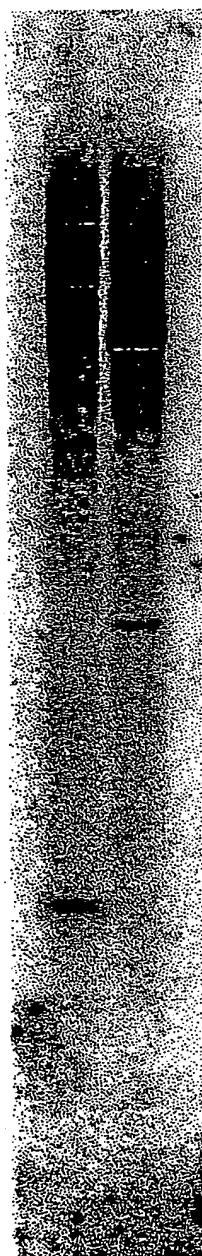
PBM

SSVV

HC2A -----
 KIAA -----
 rat -----
 HC4 CVTLPHEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVI FNSRFYRSWGK
 HC1 EVL-----
 HC3 SAEV-----
 HC5 -----

HC2A -----
 KIAA -----
 rat VHIFF
 HC4 -----
 HC1 -----
 HC3 -----
 HC5 -----

HinDIII
Eco RI



← ~ 4.5 kb

← ~ 1.85 kb

genomic DNA

Pst I
Eco RI



← ~ 4.5 kb

← ~ 1.85 kb

BAC 6 DNA

Fig. 7

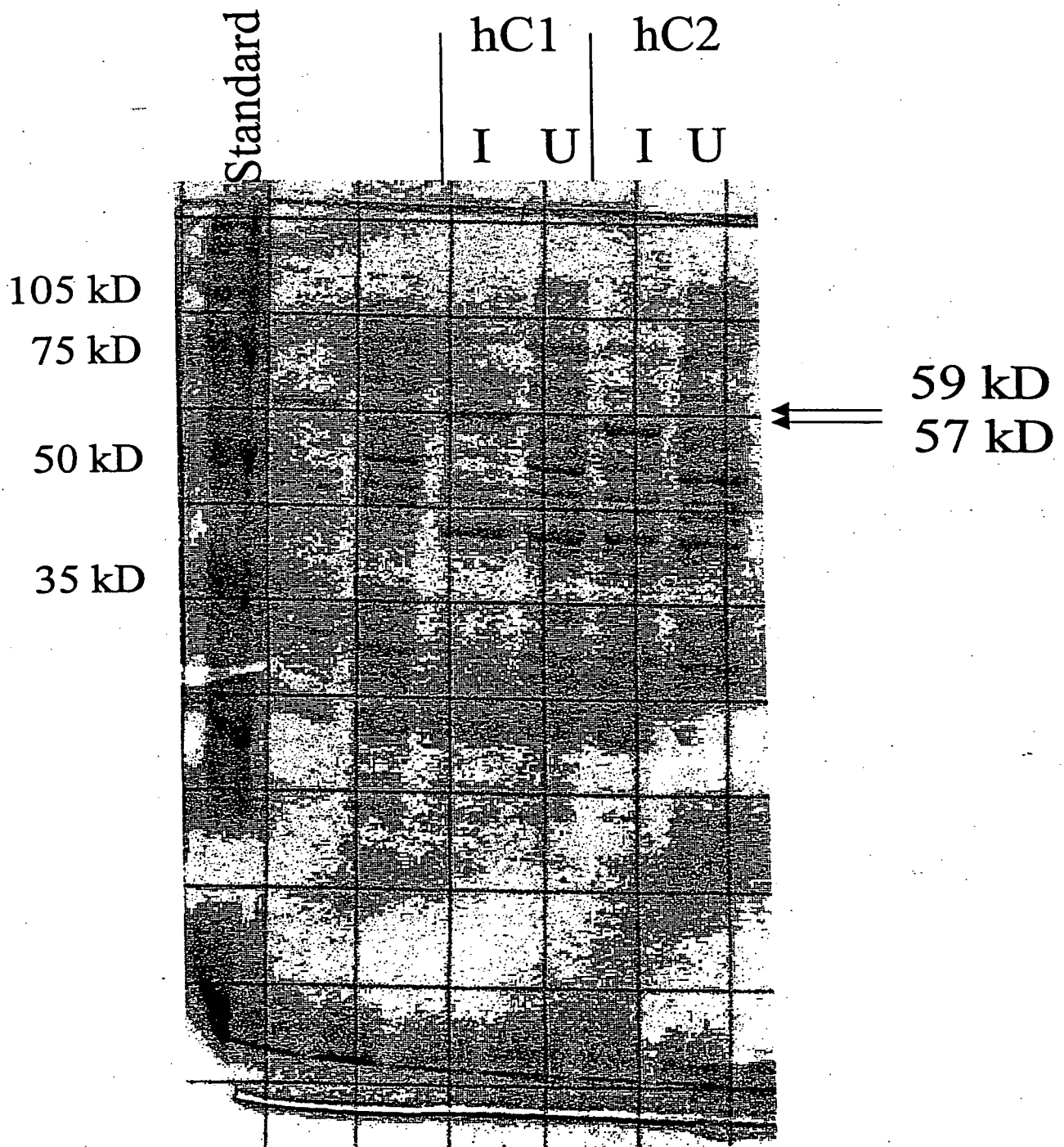


FIG. 8

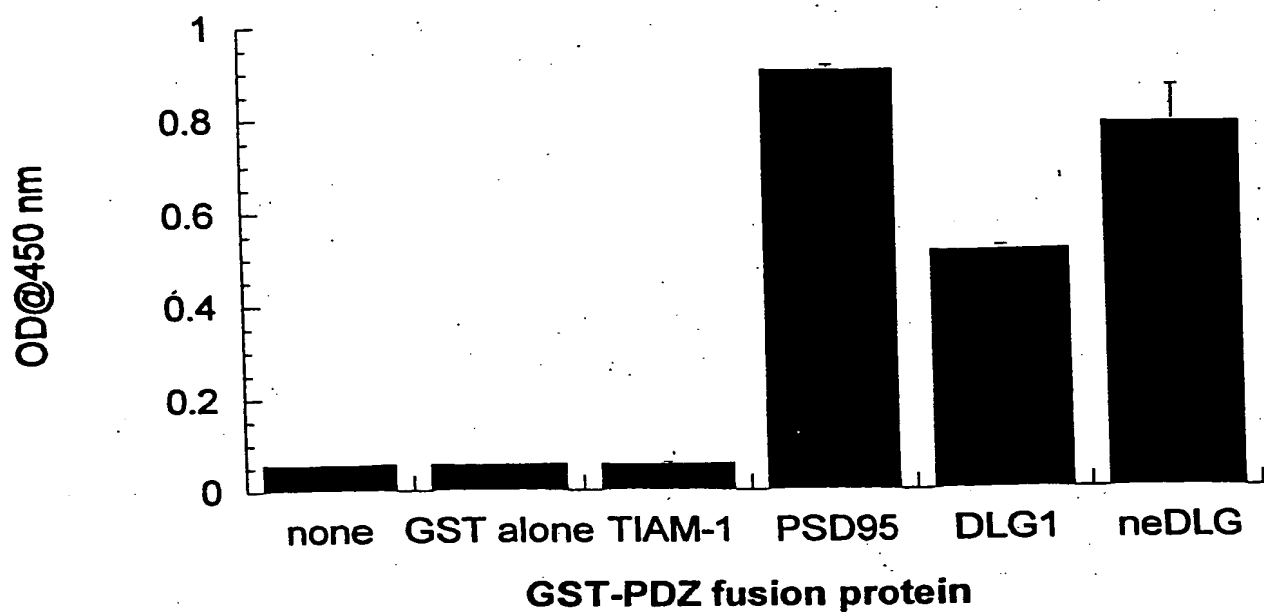


Fig. 9A

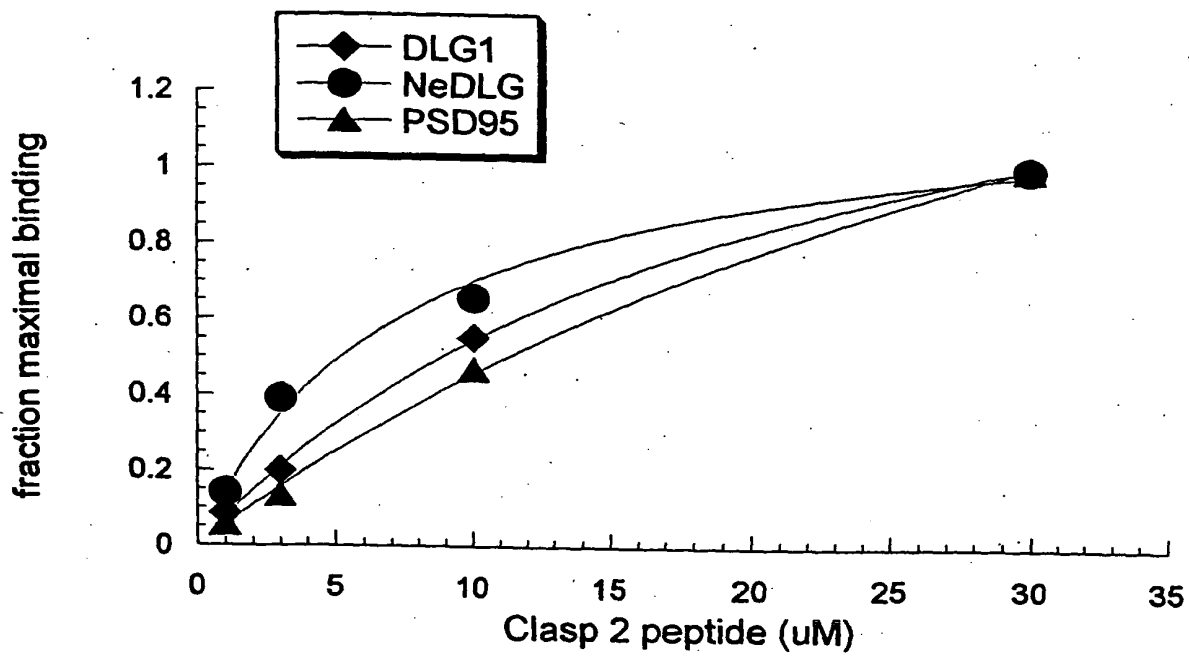


FIG. 9B

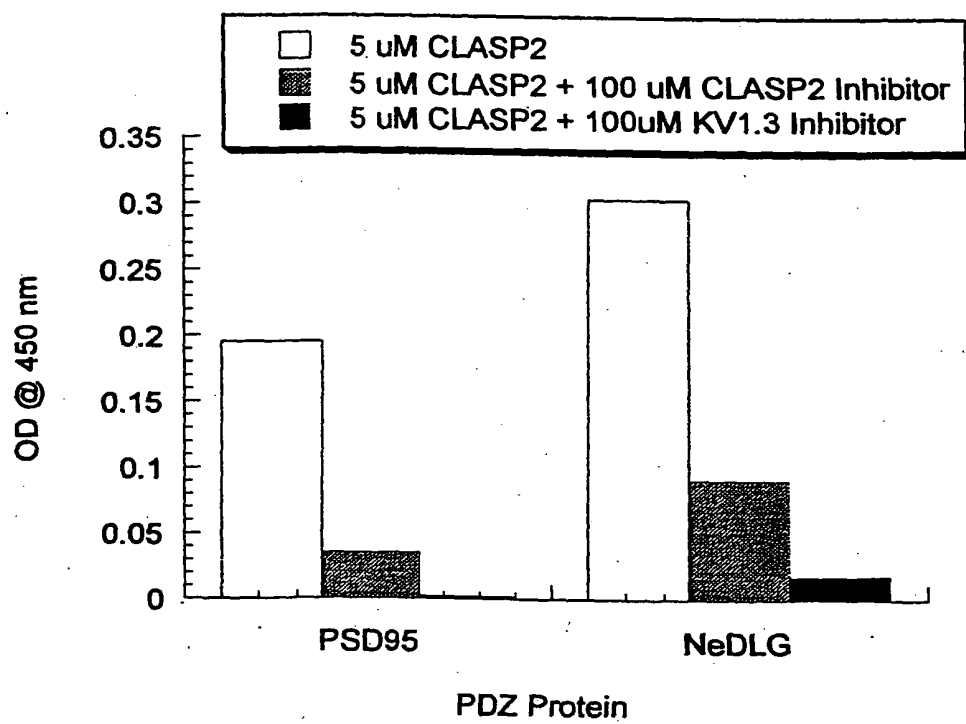


Fig. 9C

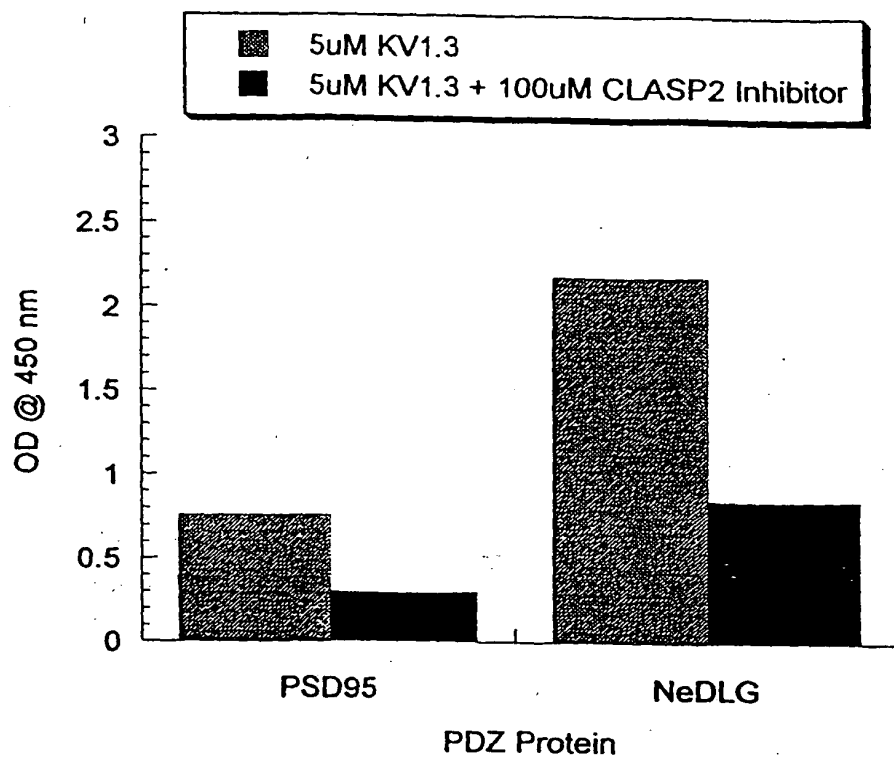


FIG. 9D

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC 80
81	GAATTCGGCA	CGAGTITTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC 160
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT 240
241	GTCTGTGAAA	CCCAAGTTGG	CTACTCTCTG	CTTCCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC 320
321	GGTCTCGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT 400
401	GGGTAGATGG	AGGCAAGCCA	TGCTGAAAA	TTTCCACTCA	TCGTGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA 480
481	ATTTTTTCCA	GTACTGTCTAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG 560
561	CATGCCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC 640
641	ACAGGAAGAA	GTCCGCGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TGGAGAGGCC 720
721	ACTTGAGGTC	ATATGTTAAG	TACGGGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG 800
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT 880
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCAATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTT 960
961	CTGCATCCTA	TCATCATGCA	GCGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA 1040
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT 1120
1121	CAAGCAGATG	AACAACCTACA	TTAGCTGTTT	GCTCTCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC 1200
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTGTGAACCT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA 1280
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG 1360
1361	GACGACCTC	CAGGAGTTCC	GGGAGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG 1440
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTGT	TTGGTCTGTG	GATTGAAAAC 1520
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAAACGCGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT 1600
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCCGCA	GAAGGGAAGC	ACCTCTGGCA	ACAGCTGCA	CAAGGACCTG	CTGGGCGCCA 1680
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAC	GTGAGAAGAG	CAATTCCTCT	GATAAGCACC	AGGATCTCTC 1760
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAAGGAATA	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA 1840
1841	CACATTGGGA	AATTCOGTGG	TTCCGTGTGA	TAAACTTGAC	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA 2000
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGAGCCCAT 2080
2001	ATATCTGAAG	CTTGCTTCCA	CCAGTTCAG	TACATGGGGA	AACAGAAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG 2160
2081	AGTTCAATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	CCACTCGGAC	GCAGATGTTT	TGCACCACTC	ATTACTTGAA 2240
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG	CGCTTTCTCT	ATTTACATTG	GCGTTTAAAG	ACCAGCTCTT 2320
2241	GCCAAACATG	CTACTGAGGT	TTGCCGTGCA	GCTCTGGACA	GATGCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA 2400
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC 2480
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTA	GGTCCCTAAT	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CTCCAGCTT 2560
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGCTGTA	AAGAAGTCTT	TTGTCCGGAG	ACATTTGCAA	GTCATCATAT 2640
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AACCAAGTTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG 2720
2641	CTGTACAGCA	GCTGATAGCA	GACGTGTGTT	GCAATGGGGA	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	TCCAGCTGCT 2800
2721	GCCAAACAGT	ACCGGCTTAT	TAAAGCACACC	AGCTTCTCCT	GAGATGTGCT	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT 2880
2801	AATGGCCACC	GCCGAGATGA	AGGAGCATGA	GAACGACCCA	GTGGCCGAGG	ATCCATGTCA	AAAATGGCGA	TCTCTCAGAG 2960
2881	ATGCCAGCAC	GCCGAGCTC	AGGAAGACGT	GGCTCGACAG	AATATCTCAC	ACGGAAGAGG	GTGTTTAGAG	AAGGATGCAC 3040
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCCA 3120
3041	CGCCTTCAGG	GTCAATTACC	CAAAACATCGA	CGAGGAGGCC	TCGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCGCCGAC 3200
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCCGAGA	ATTCTTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA 3280
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG 3360
3281	GGAACCCAAA	CTCACACCCG	TGTCGGAAAT	TTCTCAGAGA	TCGTGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC 3440
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	CAGAGTTTGA	GAGATCCCAC	AACATCCCGC	GCTTCATGTT 3520
3441	ATCCCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA 3600
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC 3680
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTA	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT 3760
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA 3840
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	AGTTTTCAGG	CAATTTGTGG	AAGCTTGCGG	TCAAGCCTTA 3920
3841	CAAAAGGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA 4000
3921	GCGGTAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT 4080
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC 4160
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA 4240
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA 4320
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAATAAAG	CAAAGTTTTT	ATTGTGCTTT	AACAAAGGTG	TGGTAGACAC 4400
4321	AGAAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG 4480
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GGGACCTTTT	TGCTTCGACT	CGTGCCGGAA	ATCTGATCGT 4560
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCCTG	TTGTATGACT	AGGATTGTG	CTATTATCTC	ATTCAACAAC 4640
4561	AATCAGGGTA	CAGAACCTTAC	TAGTTTGTGC	TAGGAGTATG	TTGATCCGCT	ACTGCCCTTA	AGTCAGAACT	TTGTCAATTA 4720
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	CATTTTTAAT	ACTCAATGCG	GCTTATGCAT	TAAGTTTAAAT 4800
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTCTTA	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA 4880
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT				4898
4881	TGTATACAAG	TCCTTTACT						

FIG. 10A

	10	20	30	40	50	60	70	80
1	MEGHVMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAOCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK 80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHAAE	TVVNM LMPHI	TOKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ 320
321	RINV RDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQSSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKMSDDA	LFTYWNKAST	SELMOFFTIS 480
481	EVCLHQFOYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQS LLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRFOQ	SLSIINN CAN 720
721	SDRLIKHTSF	SSDVKD LTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKN GDLSEAA 800
801	MCYVHV TALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIPIIYEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISORLL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQKLQGS	VSVQVNAGPL	AYARAFDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGOALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV 1194

FIG. 10A (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCCCC	GAGGTGACG	GTATCGATAA	GCTTGATATC
81	GAATTCGGCA	CGAGTITTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAAT	AGAGTTGCCC	ACTCAGCTGC
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
321	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTTAAAT
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA
481	ATTTTTTTTCA	GTACTGTCTAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTC	CGAGTCTTCA	CCAGAGCCAC
641	ACAGGAAGAA	GTGCGGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
801	ACCAAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT
881	CTTTGATGTA	CTGATCAAAAT	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTGAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
1041	GAGGCATCTA	AGAAGCGGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT
1121	CAAGCAGATC	GAACACTACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGG	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATAACAA
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCCTCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTCTG	TTGGTCTGCT	GATTGAAAAC
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
1601	ACCAGCTGTG	AATCCGCTGG	TGACGCGCGA	GAAGGGAAAG	ACCTCTGGAC	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
1681	TCTCCGGCAT	TGCTTCTTCA	TATACAACCT	CAACTCCAAC	CATCAACAGT	GTGAGAAATG	CTGATTTCAG	AGGATCTCTC
1761	ATAAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
1841	CACATTGGGA	AATTCGGTGG	TTCCGTGTGA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
1921	TCTTAAAGAG	CATGTCTGAT	GATGCTTTTG	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTATGGA	TTTTTTTACA
2001	ATATCTGAAG	TCTGCCCTGAG	CCAGTTCCAG	TACATGGGGA	AGGCAAGGCT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
2081	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAG	GCAGATGTTT	TGCACCAGTG	ATTACTTGAA
2241	GCCAAACATTG	CTACTGAGGT	TTGCCCTGACA	GCTCTGGACA	CGCTTTCTCT	ATTTACATTG	GCCTTTAAGA	ACCAGCTCCT
2321	GGCCGACCAC	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTAA	GGTCCCTAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGCTGTA	ACTCAAGCT	GAGCTCCATC	AGGACGGAGG	CTCCCCAGCT
2561	GCTCTACTTC	GAACATAATC	ACAACCTTGA	TTACACTGGA	AAGAAGTCTC	TTGTCCGGAC	ACATTGTCAC	GTCATCATAT
2641	CTGTGAGCCA	GCTGATAGCA	GACGTTGTTG	GCATTGGGGA	AACCAGATTG	CAGCAGTCCC	TGTCCATCAT	GCACAACTGT
2721	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GCACCGTGCT
2801	AATGGCCACC	GCCAGATGTA	AGGAGCATGA	GAACGACCCA	GAGATGCTCG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
2881	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAAATGGCG	TCTCTCAGAG
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAG	AAGGATGAC
3041	CGCCTTCAGG	GTCAATACCC	CAAACATCGA	CGAGGAGGCC	TCCATGTATG	AAGACGTGGG	GATGCAGGAT	GTCCATTCCA
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCCGAC
3201	ATCTACAAAC	TTATCATCCC	CATTATAGAG	AAGCGGAGGG	ATTCTTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTGGGA	TAAATTTGGT	TCTGAAAATG
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACGTC
3441	ATCCCCCTTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT
3521	TGAGATGCCA	TTTACGCAGA	CCGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAACG	GCGCACCATC	CTGACAGCCA
3601	TACACTGCTT	CCCTTATGTG	CCCTGTCTAT	TCCCTGTCTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGCGAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AAGTCAGCT
3761	CAAACCTCCAG	GGCAGCGTGA	GTGTTTCAGG	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA
3841	CAAAGCGATA	TCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGGGG	TCAAGCCTTA
3921	GGGTTAAAGC	AACGCTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGAA
4001	GGAGCTTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT
4081	TCAACGCCAT	CAGTGGGACT	CCRAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTCTGTGT	ATTACATCTC
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCTG	GGGACCTTTT	TGCCCTGACT	CGTGCCGGAA	ATCTGATCGT
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA
4721	TCATCGACTC	CGGACCGGTC	ATATATGTAT	TACATTTCTA	CATTTTTTAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA
4881	TGTATACAAG	TCTTTACT						

	10	20	30	40	50	60	70	80
1	MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEFYVASE	YKTVHEELTK 80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHA AE	TVVNMLMPHI	TQKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	OLDYSLTDEF	CRNHFLVGLL	LREVG TALQE	FREVRLIAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LFGLLIENVQ 320
321	RINV RDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLLG	AISGLASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSN SLDK	HQSSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKSM SDDA	LFTYWNKAST	SELMDFFTIS 480
481	EVCLHQFOYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMHARLQQ	LGSLDN SLTF	NHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRFOQ	SLSIINN CAN 720
721	SDRLIKHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDSMARIH	VINGDLSEAA 800
801	MCYVHV TALV	AEYLTRKGVF	RQGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADTY 880
881	KLIPIY EKR	RDFFED EDGK	EYTYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQLKLQGS	VSVQVNAGPL	AYARAF LDDT	NTKRYPDNKV	KLLKEVFRQF	VEACQALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTP T	STMVHGMTSS	SSVV 1194

FIG. 10B (cont.)

10	20	30	40	50	60	70	80
AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC
GAATTCGGCA	CGAGTTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAATAA	AGAGTTGCCC	ACTCAGCTGC
ATGAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTGAG	CTGTGACAA	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT
GTGCTTGAAA	CCCAAGTTGG	CTACTCTGG	CTTCCCCCTC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT
GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA
ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCC	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG
CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCTCTAA	CCAGCTGTTC	CGAGTCTCTA	CCAGAGCCAC
ACAGGAAGAA	GTCGGGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TTTGAATACA	AGACAGTGCA	TGAAGAACTG
ACCAAATCCA	TGACCAAGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCCG	CAACAACTA	CTGAGGTACT	CATGGTTTTT
CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC
CTGCACTCTA	TCATCATGCA	GCGGAAACCG	TTGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
AGGGCATCTA	AGAAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATGGACAGGG	GCTTTGTCTT
CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCTTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC
GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTGAACCTT	ACCAATGGCA	TTTGGAAAAG	GCAGGATTC	AGATATCCAA
GACCTCCAGC	TTGACTACTC	ATTAAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GCGAGGTGGG
GACAGCCCTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTGCT	CTGCTCTGTT	TTGGTCTGCT	GATTGAAAAC
GTCCAGCGGA	TGCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCTGT	AAGGATGAAT	CCCTGGCTCT
ACCAGCTGTG	AATCCGCTGG	TGACGCGCA	GAAGGGAAGC	ACCTTGAGCA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC
ATAAGCACAG	ATTGCGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAGAG	CAATTCCTCG	GATAAGCACC	AACAAGTAG
CACATTGGGA	AATTCCTGGG	TTGCGTGTGA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
TCTTAAAGAG	CATGCTGTGAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA
ATATCTGAAG	TCTGCTGCA	CCAGTTCCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCTG	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
GCAGCTTGG	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCATG	ATTACTTGAA
GCCAACTTG	CTACTGAGGT	TTGCCGTGAC	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	GCGTTTAAAG	ACACAGCTCT
GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
CGGCTTTAAA	AAATGCTCTC	ACTGCCTTAA	GGTCTTTAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CTCTCCAGCT
GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTTGA	AAGAAGTCTT	TTGTCCGAGC	ACATTTGCAA	GTCTCATAT
CTGTGAGCCA	GCTGATAGCA	AGAGTTGTTG	GCATTGGGGA	AACCAAGATC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG
GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	GACCGGTGCT
AATGGCCACC	GCCCAGATGA	AGGAGCATGA	GAACGAGCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
ATGCCAGCAG	GCCCAGACTC	AGGAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGGGA	TCTCTCAGAG
GCCAACTGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACCGAAAGGC	GTGTTTAGAC	AAGGATGCAC
CGCCTTCAGG	GTCAATTACC	CAACATCTGA	CGAGGAGGCC	TCCATGATGG	AAGAGCTGGG	GATGCAAGGAT	GTCCATTTC
ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGGCCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCGCGAC
ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCCGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
GGAAACCCAA	CTCACACCGC	TGTCCGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAAAT
TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACTGC
ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT
TGAGATGCCA	TTTACGAGA	CCGGGAAGAG	GCAGGCGGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA
TACTGCTCT	CCCTTATGTT	AAGAAGCGCA	TCCCTGTCT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCTCT	GGCCGAGGTG	GACATGATCA	AAGTGCAGCT
CAAACTCCAG	GGCAGGTGTA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGGAGCT	TTTCTTAGAT	GATACAAACA
CAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCA	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA
GCGGTAACG	AACGCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCTGCT	GAGGAGAAGA	CGAGCGCTTT	ACCGAATTCC	CTTCACTCT
TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTT	ATTACATCTC
ATGGCCCGTG	TGTGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGCTTT	AACAAAGGTG	TGTTAGACAC
TCTTGAGCTG	GACTTAGATT	TTATTTCTCC	TTGCAGAGTA	GTGTAGAAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTG	GGGGACCTTT	TGCTCGACT	CGTCCGGGAA	ATCTGATCGT
AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTTGTA	CTATTATCTC	ATTCAACAAC
ATAGAGCAAG	AATAGTGAGC	TAAGTGAGCT	AGACACTCAA	TCTGATGACT	ACTGGCTTCA	AGTCAGAACT	TGTTCAATTA
TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	TTATCCGCT	ACTCACATGG	GCTTATGCT	TAAGTTTAA
TGTGATAAAT	TTGTGCTGCT	CCAGTATATG	CAATACACTT	CATTTTAAAT	TTCTTGTCAT	AAAAATGTGC	AATATGGAGA
TGTATACAAG	TCCTTACT			TAATGGTTTA			
10	20	30	40	50	60	70	80
							80
							160
							240
							320
							400
							480
							560
							640
							720
							800
							880
							960
							1040
							1120
							1200
							1280
							1360
							1440
							1520
							1600
							1680
							1760
							1840
							1920
							2000
							2080
							2160
							2240
							2320
							2400
							2480
							2560
							2640
							2720
							2800
							2880
							2960
							3040
							3120
							3200
							3280
							3360
							3440
							3520
							3600
							3680
							3760
							3840
							3920
							4000
							4080
							4160
							4240
							4320
							4400
							4480
							4560
							4640
							4720
							4800
							4880
							4898

Fig. 10C

	10	20	30	40	50	60	70	80
MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRV I HV	VAQCHEEGLE	SHLRSYV KYA	YKAEPPY VASE	YKTVHEELTK	80
SMTTILKPSA	DFLT SNKLLR	YSWFFFDVLI	KSMACHLIEN	SKVKLLRNQR	FPASYHHAAE	TVVMMLMPHI	TQKFGDNPEA	160
SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL	240
QLDYSLTDEF	CRNHFLVGLL	LREVGTA LQE	FREVRLIAIS	VLKQLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVO	320
RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLLG	AI SGIASPYT	TSTPNINSVR	NADSRGSLIS	400
TDSGNSLPER	NSEKSNSLDK	HQQSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKMSDDA	LFTYWNKAST	SELMOFFTIS	480
EVCLHQFOYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMHARLQO	LGSLONSLTF	NHSYGHSDAD	VLHQSLLEAN	560
IATEVCLTAL	DTLSLFTLAF	KNOLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640
AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRPOQ	SLSIINN CAN	720
SDRLIKHTSF	SSDVKDLTKR	IRTVMATAQ	MKEHENDPEN	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAR	800
1 MCYVHV TALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADTY	880
1 KLIPIY EKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVMIQDSGK	VNPKOLD SKY	AYIQVTHVIP	960
1 FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKROGGVE	EOCKRRTILT	AIHCFFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040
1 EMSKKVAELR	QLC SSAEVDN	IKLQWKLGQS	VSVQVNAGPL	AYARAFLODT	NTRKYPDNKV	KLLKEVFRQP	VEACGQALAV	1120
1 NERLIKEQDL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV	1194

FIG. 10C (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCCCC	GAGGTGACGG	GTATCGATAA	GCTTGATATC
2	GAATTTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCCC	ACTCAGCTGC
3	ATGAAAGAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT
4	GTGGTTGAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
5	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT
6	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA
7	ATTTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG
8	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC
9	ACAGGAAGAA	GTGCGGTTTA	ACGTGACTCG	GGTCTATTAT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
10	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAAGCTG
11	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT
12	CTTTGATGTA	CTGATCAAA	CTATGGCTCA	GCAATTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTT
13	CTGCATCTTA	TCATCATGCA	CGGGAACCG	TGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
14	GAGGCTCTTA	AGAACGGGAA	TCTATGCCCT	GCTGTCTTCA	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT
15	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAAGTTT	GAATTTCTCC
16	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGGCA	TTTGGAAAAG	GCAGGATTTA	AAGATACCAA
17	GACCTCTAGC	TTGACTCTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GCGAGGTGGG
18	GACAGCCCTC	CAGGAGTTTC	GGGAGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAGAAACCT	GCTGATAAAG	CATTCTTTTG
19	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACGCTCTAC	CTGCCCTGCT	TGGTCTGCT	GATTGAAAAC
20	GTCCAGCGGA	TCAATGTGAG	GGATGTGTC	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
21	ACCAGCTGTG	AATCCGCTGG	TGACGCGCA	GAAGGGAAGC	ACCTTGAGCA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
22	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCCAG	AGGATCTCTC
23	ATAGCACAG	ATTCCGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
24	CACATTGGGA	AATTCCGTTG	TTCCGCTGTA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
25	CTTTAAAGAG	CATGCTGAT	GATGCTTTGT	TTACATATTG	GAACAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA
26	ATATCTGAAG	CTTGCTGCA	CCAGTTCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
27	AGTTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	ACACAGACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
28	GCAGCCTTGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCACTG	ATTACTTGAA
29	GCCAAACATT	CTACTGAGGT	TTGCCGTACA	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	GGGTTTAAAG	CAGTCTGAAA
30	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGCTTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
31	CGGCTTTAAA	AAATGTCTTC	ACTGCCTTAA	GGTCTTAA	TTATAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
32	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	ACAACCTTGA	TTACACTGGA	ACTCCAAGCT	GAGCTCCATC	CTCCAGCT
33	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AGAAGTCTCT	TTGTCCGGAC	ACATTTGCAA	GTCTCATAT
34	CTGTGAGCCA	GCTGATAGCA	GAGCTTGTGT	GCAITGGGGA	AAACAGGCTT	CAGCAGTCCC	TGTCCATCAT	CAACACTGTT
35	ATGTGTGCGG	ACCGGCTTAT	TAAACACACC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	ACACGCTGCT
36	AATGCCACCC	GCCAGATGTA	AGGAGCATGA	GGCTCGACAG	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
37	ATGCCAGCAC	CGCCGAGCTG	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGGGA	TCTCTCAGAG
38	GCCCAATGTT	GCTATGTCCA	CGTAACAGCC	CTAGTGGGAG	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAC	AGGATGACAC
39	CGCCTTCAGG	GTCAATACCC	CAAAACATCGA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGACAGAT	GTCCATTTCA
40	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTCCGACGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATCCCGAC
41	ATCTATCAAA	TTATCTATCC	CATTATAGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAAGAGT	ATATTTACAA
42	GGAAACCCAA	CTCACACCC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG
43	TCAAAATGAT	ACAAGATTCT	GGCAAGGTCA	ACCTTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCAGCTC
44	ATCCCTTCTT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT
45	TGAGATGCCA	TTTACGCGA	CGGGGAAGAG	GCAAGGGGCGG	GTGGAAGAGC	AGTGCAAACG	GCGCACCATC	CTGACAGCCA
46	TACACTGCTT	CCCTTATGTT	AAGAAGCGCA	TCCCTGTCTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGTGGCCC
47	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	CCACTAGCAT	ATGGCGGAGC	TTTCTTAGAT
48	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGGCGGAGC	TTTCTTAGAT	GATACAAACA
49	CAAGCGGATA	TCCTGACAA	AAAGTGAAGC	TGCTTAAGGA	AGTTTTCAGG	CAATTGTGG	AAGCTTGGCG	TCAAGCCTTA
50	CGCGTAAACG	AACGCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACACAGGG	AAATGGCGAA
51	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT
52	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC
53	ATGGCCCGTG	TGTGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
54	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
55	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAAGTTTT	ATTGTGCTT	AACAAAGGTG	TGGTAGACAC
56	TCTTGAGCTG	GACTTAAATT	TTATTTCTCC	TTGCAGAGTA	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
57	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCCTG	GGGGACCTTT	TGCCCTGACT	CGTGCCGGAA	ATCTGATCGT
58	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTTGTG	CTATTATCTC	ATTCAACAAAC
59	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTATATGAT	ACTGAGTGG	GCTTATGCAT	TAAGTTTAAAT
60	TCATGCACTC	CGGACGGTGA	ATATATGTAT	TACATTTCTA	TGATATAAT	ACTCACATGG	AAAAATGTGC	AAATATGGAGA
61	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTGTGCT	AAAAATGTGC	AAATATGGAGA
62	TGTATACAAG	TCTTTACT						

	10	20	30	40	50	60	70	80
MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNTRVIIHV	VAQCHEEGLE	SHLSYVVKYA	YKAEPTVASE	YKTVHEELTK	80
SMTTILKPSA	DFLTSTNKLRL	YSWFFFDVLI	KSMAQH LIEN	SKVKLLRNQR	FPASYHHA AE	TVVNMLMPHI	TOKFGDNPEA	160
SKONANHS LAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPNLMPMPG	KGRIQRYQDL	240
QLDYSLTDEF	CRNHFLVGLL	LREVGTAQOE	FREVRLIAIS	VLKXLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ	320
RINVRDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLG	AI SGIASPYT	TSTPNINSVR	NADSRGSLIS	400
TDSGNSLPER	NSEKSNLSDK	HQOSSTLGNS	VVRCDKLDQS	EIKSLMCFI	YILKMSDDA	LFTYWNKAST	SELMDFFTIS	480
EVCLHQFOYM	GKRYIARNOE	GLGPIVHDRK	SQTLFVSRNR	TGMMHARLQQ	LGSLDNLTF	NHSYGHSDAD	VLHQSLLEAN	560
IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC	640
AALCYEILKC	CNSKLSSTRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRPQQ	SLSIINNCAN	720
SDRLIKHTSF	SSDVKDLTKR	IRTVMATAQ	MKEHENDPEN	LVDLQYSLAK	SYASTPELRK	TWLD SMARIH	VKNGDLSEAA	800
MCYVHV TALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASN	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY	880
1 KLIIP IYEKR	RDFFEDEDGK	EYTYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP	960
1 FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID	1040
1 EMSKKVAELR	QLCSSAEVDM	IKLQKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQP	VEACGQALAV	1120
1 NERLIKEDQL	EYQEEPMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPSNLH	IFNAISGTPT	STMVHGMTSS	SSVV	1194

FIG. 10D (cont.)

10	20	30	40	50	60	70	80
ATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACGGG	GCCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC
AATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC
TGAARAAGCA	CCACTGTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGGAT
TCGTTGAAA	CCCAAGTTGG	CTACTCTCG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGT	ACAAGCGAGC	AGCACATCCC
CTCTCGCGG	AACTTCTCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTTAAAT
GGTAGATTG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA
TTTTTTTCA	GTACTGTCTAG	AAAAACGAA	CTGGAGCCCA	AGCCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG
DATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC
ACAGGAAGAA	GTGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TGGAGAGGCC
ACTTGAGGTC	ATATGTTAAG	TACGGGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
ACCAAATCCA	GTCTCAAGCCT	TCTGCGGATT	TTCTGCTGGA	TCTCTACCAG	CAACAAACTA	CTGAGGTACT	CATGGTTTTT
CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA	GAGAATCTCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC
CTGCATCCTA	TCATCATGCA	GCGGAAACCT	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
GAGGCACTCA	AGAAACGGAA	CTATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACCTTC	ATOGACAGGG	GCTTTGCTCT
CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCTGGA	GACCCAAAGA	CCCTCTTGA	ATACAAGTTT	GAATTTCTCC
GTGTAGTTG	CAACCATGAA	CATTATATTC	CGTTGAACCT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA
GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GAGTTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
GACAGCCCTC	GAGGAGTTCC	GGGAGGTCGG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTGT	TTGGTCTGCT	GATTGAAAAC
GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGCTCT
ACCAGCTGTG	AATCCGCTGG	TGAAGCGGCA	GAAGGGAAGC	ACCTCTGACA	ACAGCTTGA	CAAGGACCTG	CTGGGCGCCA
TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCCAG	AGGATCTCTC
ATAAGCAGAG	ATTCCGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
CACATTGGGA	AATTCCTGG	TTCCGTGTGA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
TCTTAAAGAG	CATGTCGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACTTATGGA	TTTTTTTACA
ATATCTGAAG	TCTGCCCTGA	CCAGTTCGAG	TACATGGGGA	AGCCATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGAGCCCAT
AGTTCTATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
GCAGCCTGGA	TAACCTCTCT	ACTTTTAAAC	CAGTATATGG	CCACTCGGAC	GCAGATGTTT	TGCCACCATC	ATTACTTGAA
GCCAACTATG	CTACTGAGGT	TTGCCCTGACA	GCTCTGGACA	CGCTTTCTCT	ATTTACATG	CGCTTTAAGA	ACCAGCTCTT
GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTGTTTTCT	TCAAAAACAT	CAGTCTGAAA
CGGCTTTAAA	AAATGCTCTC	ACTGCCCTTAA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
ATGTGTGGGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	ACTCCAAGCT	GAGCTCCATC	AGGAAGGAGG	CTCCTCCGAC
GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	AAGAACTCCT	TTGTCCGGAC	ACATTGCAA	GTATCATAT
CTGTACAGCA	GCTGATAGCA	CAGCTTTGTT	GCAATGGGGA	AACAGATTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG
GCCAAACAGT	ACCGGCTTAT	TAAGCACACT	AGCTTCTCCT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC	CAGCGTGTCT
AATGGCCACC	GCCAGATGTA	AGGAGCATGA	GAAAGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
ATGCCAGCAC	GCCCGAGCTG	AGGAAGAGCT	GGCTGACAG	CATGGCCAGG	ATCCATGTCA	AAAATGGOGA	TCTCTCAGAG
GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	CTCATCTCAT	ACOGAAAGGC	GTGTTTAGAC	AAGATGCCAC
CGCCTTCAGG	GTCATTACCC	CAAAACATGA	CGAGGAGGCC	TCCATGTATG	AAGACGTGGG	GATGCAGGAT	GTCCATTTCA
ACGAGGATGT	CTCTGTGAG	CATTTATGAG	AAGCGGAGGG	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCGGAC
ATCTACAAAC	TTATCATCCC	CTCTGTGAG	TTCTCAGAGA	ATTCTTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTTACA
GGAACTCCAAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCTTTAAAC	TGTACTCGGA	TAAATTTGGT	CTGAAAAATG
TCAAAATGAT	ACAGGATTTCT	CGAAAGGTCA	ACCCATAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT	GACTCACTCT
ATCCCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCCAT	AACATCCGCT	GCTTCATGTT
TGAGATGCCA	TTTACGCGAG	CCGGGAAGAG	GCAGGGGGGG	GTGGAAGAGC	AGTGCAAAAG	GCGCAACATC	CTGACAGCCA
TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT
CAAACCTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGGAGC	TTTCTTAGAT	GATACAAACA
CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA
GGGTTAAACG	AACGTCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
GGAGCTTTCT	GAATCATGCG	ATGAGCAGAT	CTGCCCTCT	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT
TCAACGCCAT	CAGTGGGACT	CCAAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTGCTCTT	CGGTGCTGTG	ATTACATCTC
ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT	AGGAGTTGTA
AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTC	ATTGTGCTCT	AACAAAGGTG	TGGTAGACAC
TCTTGAGCTG	GACTTAGAAT	TTATTTCTCC	TTGCAGAGTA	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTTCTGG
ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGAGGCTTG	GGGGACCTTT	TGCCCTGACT	CGTGCCGGAA	ATCTGATCGT
AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGATGACTT	AGGATTTGTG	CTATTATCTC	ATTCAACRAAC
ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TAAATCCGCT	ACTGGCTTCA	GCTTATGCA	TAGTTTAAAT
TCATCGACTC	GGGAGCGGTC	ATATATGTAT	TACATTCTTA	CAITTTTAAAT	ACTCACATGG	GCTTATGCA	TAGTTTAAAT
TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTGTGCTAT	AAAAATGTGC	AATATGGAGA
TGTATACAG	TCITTACT						
10	20	30	40	50	60	70	80

FIG. 10E

10	20	30	40	50	60	70	80
VMIAFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPIVASE	YKTVHEELTK 80
ILKPSA	DFLTSHKLLR	YSWFFFDVLI	KSMACHLIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMIMPHI	TOKFGDNPEA 160
NHSLAV	FIKRCFTFMD	RGFVFKQIDN	YISCFAPGDP	KTLFEYKFEF	LRVVCHHEHY	IFLNLMPPFG	KGRIOKYODL 240
SLTDEF	CRNHFLVGLL	LREVGTAQOE	FREVRLLAIS	VLKOLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVO 320
RDVSPF	PVNAGMTVKD	ESLALPAVRP	LVTPOKGSTL	DNSLHKDILG	AISGLASPTT	TSTPNINSVR	KADSRGSLIS 400
SNLPER	NSEKSNSLDK	HQOSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMDDA	LFTYWNKAST	SELMOPFTIS 480
LHQFOYM	GKRYIARNQE	GLGPVHDKK	SOTLPVSRNR	TGMHARLQO	LGSIDNSLTF	NHSYGHSDAD	VLHQSLLEAN 560
EVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFV	YLCFLQKHQS	ETALQNVFTA	LRSLTYKPPS	TFYEGRADMC 640
CYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGK	SFVRTHLQVI	ISVSQIADV	VGIGETRPQO	SLSIDNRCAN 720
LKHTSF	SSDVLDLTKR	IRTVIMATAQ	MKEHENDPEM	LVDLOYSIAK	SYASTPELRK	TWLDSMARIE	VKNGDLSEAA 800
VHVTALV	AEYLTRUGVF	ROGCTAFRVI	TPMIDEEASM	MEDVGMQDVH	FNEDVIMELL	EQCADGLWKA	ERYELIADTY 880
IPIYEKR	RDFFEDEDGK	EYTYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVMQIDSGK	VNPKDLDSKY	AYIQVTHVIP 960
DEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKROGGVE	EQCKRRTILT	AIHCFFPYVK	RIPVMYQHHT	DLNPIEVAID 1040
SKKVAELR	QLCSSAEVDM	IKLQIKLQGS	VSVQVRAGFL	AYARAPLDDT	NTRYPDNKV	KLLKEVFRQP	VEACQALAV 1120
RLIKEDQL	EYQEDMKANY	REMAKELSEI	MHEQICPLEE	KTSVLFNELH	IFRAISGTPT	STMVHGMTSS	SSVV 1194

FIG. 1DE (cont.)

	10	20	30	40	50	60	70	80
1	ATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTGACG	GTATCGATAA	GCTTGATATC
2	AAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAAAT	AGAGTTGCCC	ACTCAGCTGC
3	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCACGAA	GAAGAGGGAT
4	JTGCTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
5	GGTCTCGGCG	AACCTTCCTT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAT
6	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTACATA
7	ATTTTTTCCA	GTACTGTCAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGAGTCTG
8	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCCTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC
9	ACAGGAAGAA	GTCGCGGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
10	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
11	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCCTCACCAG	CAACAACTA	CTGAGGTACT	CATGGTTTTT
12	CTTTGATGTA	CTGATCAAA	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTT
13	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
14	GAGGCATCTA	AGAAACGCGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCITTTGCTT
15	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	GGTCTCTGGA	GACCCAAAGA	CCCTCTTGA	ATACAAGTTT	GAATTTCTCC
16	GTGTAGTGTG	CAATATATTC	CGTTGAACCT	GAGTTCTGCA	ACCAATGCCA	TTTGAAAAG	GCAGGATTCA	AAGATACCAA
17	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	TCTGATCGCC	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
18	GACAGCCCCC	CAGGAGTTCC	GGGAGGTCCG	CAAGGATAGC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
19	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTGT	TTGGTCTGCT	GATTGAAAAAC
20	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACCGGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
21	ACCAGCTGTG	AATCCGCTGG	TGAACCGCGA	GAAGGGAAGC	ACCTCTGGACA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
22	TCTCCGGCAT	TGCTTCTCCA	TATACAACTT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCCAG	AGGATCTCTC
23	ATAGACAGAG	CAAGCATGAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAAGT	CAATTCCTCT	GATAAGCACC	AACAAAGTAG
24	CACATTGGGA	AATTCCTGGG	TTCCGTGTGA	TAAACTTGAC	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
25	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTAGGA	TTTCTTACA
26	ATATCTGAAG	TCTGCCCTGA	CCAGTTCCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
27	AGTTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCTG	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
28	CGAGCCTTGA	TAACTCTCTC	ACTTTTAACC	ACAGCTATGG	CCACTCGGAC	CGAGATGTTT	TGCACCACTC	ATTACTTGAA
29	1	GGCAACATTG	CTCTGGGTAA	AAAGATTITT	CGCTTCTCTT	ATTTACATTG	GGGTTTAAGA	ACCACTCTCT
30	1	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAGATTITT	GATGCTTACC	TGTTTCTTCT	TCAAAAACAT
31	1	CGGCTTTAAA	AAATGTCTTC	ACTGCCITTA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG
32	1	ATGTGTGGGG	CTCTGGTTTA	CGAGATTCTC	AAGTGCTGTA	ACTCCAAGCT	GAGTCCATC	AGGACGGAGG
33	1	GCTCTACTTC	CTGATGAGGA	ACAACTTTGA	TTACACTGGA	AAGAAGTCTT	TTGTCCGGAC	ACATTTGCAA
34	1	CTGTACAGCA	GCTGATAGCA	GACGTTGTGT	GCATTGGGGA	AACCAGATTG	CGACAGTCCC	TGTCCATCAT
35	1	GCCAAACAGT	ACCGGCTTAT	TAAGCACACC	AGCTTCTCTT	CTGATGTGAA	GGACTTAACC	AAAAGGATAC
36	1	AATGGCCACC	GCCGAGTGA	AGGAGCATGA	GAACGACCTA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG
37	1	ATGCCAGCAC	GCCCGAGCTC	AGGAAGACGT	GGCTCGACAG	TGGACTCTGG	ATCCATGTCA	AAAATGGCGA
38	1	CGAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACCGAAAGGC	GTGTTTAGAC
39	1	CGCCTTCAGG	GTCAATTACCC	CAAACATCGA	CGAGGAGGCC	TCCATGATGT	AAGACGTGGG	GATGCAGGAT
40	1	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGGAGC	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT
41	2	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	ATTCTTTTGA	AGATGAAGAT	GGAAAGGAGT
42	3	GGAAACCCAA	CTCACACCGC	TGTCGGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT
43	51	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTTAAGGA	TCTGGATTCT	AAGTATGCAT	ACATCCAGGT
44	41	ATCCCTTTCT	TTGAGGAAAA	AGAGTTTGCA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC
45	21	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAG	GCGCACCATC
46	02	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCA	GTCCGAGCAG	CACACTGACC	TGAACCCCAT
47	81	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCCTC	GGCCGAGGTG	GACATGATCA
48	61	CAAACTCCAG	GGCAGGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCCGAGC	TTTCTTAGAT
49	41	CAAGCGATA	TCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTCAGG	CAATTTGTGG	AAGCTTGCCG
50	21	GCGGTAAACG	AACGTCTGAT	TAAAGAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG
51	01	GGAGCTTTCT	GAATCATGCT	ATGAGCAGAT	CTGCCCTCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC
52	181	TCACGCCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTT
53	61	ATGGCCCGTG	TGTGGGACT	TGCTTTGTCA	TTTGCAAAC	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG
54	141	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTTCTAT
55	122	AGAAGGTGCA	CATATTTTTC	TAAATCTCAC	TGGCAATATT	CAAGTTTTC	ATTGTTGCTT	AACAAAGGTG
56	101	TCTTGAGCTG	GACTTAGATT	TTATTTCTTC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAAAA
57	182	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCCCTG	GGGACACTTT	TGCCCTGACT	CGTCCCGGAA
58	561	AATCAGGGTA	CAGAACTTAC	TAGTTTGTCT	TAGGAGTATG	TTGATGACT	AGGATTGTG	CTATTATCTC
59	541	ATAGAGCAAG	AATAGTGAGC	TAAGTGTGCT	AGACACTCAA	TTAATCCGCT	ACTGCTTCA	AGTCAGAACT
60	721	TCATCGACTC	CGGACCGGTC	ATATATGAT	TACATTTCTA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT
61	801	TGTGATAAAT	TGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCAT	AAAAATGTGC
62	881	TGTATACAG	TCITTAAT					AATATGGAGA
	10	20	30	40	50	60	70	80

FIG. 10F

10	20	30	40	50	60	70	80
MIAFL	PTILNQLFRV	LTRATQEEVA	VNVTIRVIIHV	VAQCHEEGLE	SHLRSTYVKA	YKAEPYVASE	YKTVHEELTK 80
LKPSA	DFLTSMILLR	YSMFFFDVLI	KSMACHLIEN	SKVILLERQR	FPASYDHAAE	TVVRMLMPHI	TOKFGONPEA 160
MSLAV	FIKRCFTFMD	RGFVFKQDNN	YISCFAPGDP	KILFEYKPEF	LRVVCNHEHY	IPLNLPMPFG	KGRIOQYQDL 240
SLTDEF	CRNHFLVGLL	LREVGTAIQE	FREVLIAIS	VLQNLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ 320
RDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNLSLHDLIG	ASGIASPYT	TSTPNINSVR	NADSRGSLIS 400
NSLPER	NSEKSNLDR	HOOSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKSMDDA	LFTYWNKAST	SELMOFFTIS 480
HQFOYM	GKRYIARNQE	GLGPIVHDRK	SOTLPVERNR	TGMHARLOQ	LGSLDNLITF	RHSYGHSDAD	VLHQSLLEAN 560
VCLTAL	DTLSLFTLAF	KNOLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALJQVPTA	LRLSLTYKPPS	TFYEGRADMC 640
YEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGK	SFVRTHLQVI	ISVSQLIADV	VGIGETRPOQ	SLSIIRNCAN 720
IXHTSF	SSDVKDLTKR	IRTVLMATAQ	MKEHENDPEM	LVDLOYSIAK	SYASTPELRK	TMLDSMARIH	VKNGDLSEAA 800
HTALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM	MEDVGNQDVH	FNEDVIMELL	EQCADGLWKA	ERYELLADTY 880
PIYER	RDFEDEDGK	EYTYKEPKLT	PLSEISORLL	KLYSDKFGSE	NVMIODSGK	VNPKDLDISKY	AYIQVTHVIP 960
EKELQER	KTEFERSHNI	RRFMFEMPPT	QTGKROGGVE	EQCKRTILT	AIHCFFPYVK	RIFVMYQHHT	DLNPIEVAID 1040
KVAELR	QLCSSAEVDM	IKLQJLQGS	VSVQVWAGPL	AYARAFLODT	NTRYPDNKV	KLLKEVFRQP	VEACQALAV 1120
LIKEDOL	EYOEDMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNLSH	IFNAISGTPT	STMVHGMTSS	SSVV 1194

FIG. 10F (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTGACAG	GTATCGATAA	GCTTGATATC
81	GAATTCGGCA	CGAGTTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAAAT	AGAGTTGCC	ACTCAGCTGC
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAAC	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGAT
241	GTCGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCCTCC	TGAAAAGACGG	AAGGTTGGTG	ACAAGCGAGC	AGCACATCCC
321	GGTCTCGGCG	AACCTTCCCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAAATTAAAT
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCTGGTTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA
481	ATTTTTTCCA	GTACTGTGAG	AAAACCGAAT	CTGGAGCCCA	AGCCTTAGGA	AACGAACTTG	TAAAGTACCT	TAAGAGTCTG
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TTCTTGCCCA	CTATCTCTAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC
641	ACAGGAAGAA	GTCCGCGTTA	ACGTGACTCG	GGTCATTATT	CATGTGGTTG	CCCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACTG
801	ACCAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCCGATT	TCTCTACCAG	CAACAACTA	CTGAGGTAAT	CATGGTTTTT
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTTGATA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTC
961	CTGCATCCTA	TCATCATGCA	GCGGAAACCG	TTGTAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
1041	GAGGCATCTA	AGAACGCGAA	TCATAGCCTT	GCTGTCTTGA	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT
1121	CAAGCAGATC	AACAACCTACA	TTAGCTGTTT	TGCTCTGGA	GACCCAAAG	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	ACCAATGCCA	TTTGGAAAAG	GCAGGATTCA	AAGATACCAA
1281	GACCTCCAGC	TTGACTACTC	ATTAACAGAT	GATGTTCTGA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	TGGAGGTGGG
1361	GACAGCCCTC	CAGGAGTTCC	GGGAGGTCGG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTAC	CTGCCCTGTG	TTGGTCTGCT	GATTGAAAAA
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAA	CCTGGCTCT
1601	ACAGCTGTGT	AATCCGCTGG	TGACGCCGCA	GAGGGAAGC	ACCTTGAGCA	ACAGCTGCA	CAAGGACCTG	CTGGGCGCCA
1681	TCTCCGGCAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTCGAG	AGGATCTCTC
1761	ATAAGCACAG	ATTCGGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCAAC	AACAAAGTAG
1841	CACATTGGGA	AATTCCGTGG	TTCCCTGTGA	TAACTTTAG	CAGTCTGAGA	TTAAGAGCCT	ACTGATGTGT	TTCTCTTACA
1921	TCTTAAAGAG	CATGCTGTAT	GATGCTTTGT	TTACATTTAG	GAACAAGGCT	TCAACATCTG	AACCTATGGA	TTTTTTTACA
2001	ATATCTGAAG	TCTGCTTGCA	CCAGTTCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGACCTCAT
2081	AATGTCATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTTCCCG	AACAGAAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCAGTC	ATTACTTGAA
2241	GCCAAACATT	CTACTGAGGT	TTGCTTGACA	GCTCTGGACA	CGCTTTCTCT	ATTTTACATT	GCGTTTAAAG	CCTCGGCTCT
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGCTTACC	TTGTTTTTCT	TCAAAAACAT	CAGTCTGAAA
2401	CGGCTTTAAA	AAATGTCTTC	ACTGCCCTTA	GGTCTTAAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTGTCTGA	ACTCCAAGCT	GAGCTCCATC	AGGACGGAGG	CCTCCCAGCT
2561	GCTCTACTTC	CGCACTTAAC	AACTTTTGA	TTACACTGGA	AAGAAGTCTT	TTGTCCGGAG	ACATTTGCAA	GTCTCATAT
2641	CTGTAGCCCA	GCTGATAGCA	GACGTTGTTG	AGCTTCTCTT	AACCAAGTTC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG
2721	GCCAAACAGT	ACCGGCTTAT	TAGGACACAC	AGCTTCTCTT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	CAAGCGTGCT
2801	AATGGCCACC	AGGAGCATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
2881	ATGCCAGCAC	CGCCGAGCTC	AGGAAGACGT	AGGAGCATGA	CATGGCTCAG	ATCCATGTCA	AAAATGGCGA	TCCTCTAGAG
2961	GCAACGATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAGGCG	GTGTTTAGAG	AAGAGCTGCT
3041	CGCTTTCAGG	GTCATTAACT	CAACATCGA	CGAGGAGCCC	TCCATGATGG	AAGACGTGGG	GATGCGAGAT	GTCCATTTCA
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTCCGACGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCGCGAC
3201	ATCTACAAAC	TTATCATCCC	CATTATGAG	AAGCGGAGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
3281	GGAAACCCAAA	CTCACACCGC	TGTCGGAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCTTAAGGA	TCTGGAATCT	AAGTATGCAT	ACATCCAGGT	GACTCACGTC
3441	ATCCCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCCAC	AACATCCGCC	GCTTCATGTT
3521	TGAGATGCCA	TTTACGCAGA	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCTAT	GTACCAAGAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	TGTGCTCTCT	GGCCGAGGTG	GACATGATCA	AACATGAGCT
3761	CAAACTCCAG	GGCAGCGTGA	GTGTTCAAGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA
3841	CAAAGCGATA	TCCTGACAAT	AAAGTGAAGC	TGCTTAAAGGA	AGTTTTCAGG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA
3921	GCGGTAAACG	AACGCTGAT	TAAAGAAGAC	CAGCTCGAGT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCTCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATTCC	CTTCACATCT
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTC	ATTACATCTC
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAAATAAAG	AACAACGTTA	TTTCTTAAAC	GACTTCTTAT	AGGAGTTGTA
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAAGTTTTT	ATTGTGCTTT	AACAAAGGTT	TGGTAGACAC
4401	TCTTGAGCTG	GACTTAGATT	TTATTCTTCC	TTCAGATATA	GTGTTAGAAT	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTGT	GGGACCTTTT	TGCCCTGACT	CGTGCGGAAA	ATCTGATCGT
4561	AATCAGGGTA	CAGAACCTTAC	TAGTTTTGTC	TAGGAGTATG	TTGATGACT	AGGATTGTGT	CTATTATCTC	ATTCAACAAC
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAATTA
4721	TCATCGAATC	CGGAGCGGTC	ATATATGTAT	TACATTCTTA	CATTTTAAAT	ACTCACATGG	GCTTATGCAT	TAAGTTTAAAT
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCTAT	AAAAATGTGC	AATATGGAGA
4881	TGTATACAAG	TCTTTACT						

	10	20	30	40	50	60	70	80
1	MEGHVMI AFL	PTILNQLFRV	LTRATQEEVA	VNVTRVIIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPYVASE	YKTVHEELTK 80
81	SMTTILKPSA	DFLTSNKLLR	YSWFFFDVLI	KSMAOHLIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMIMPHI	TQKPGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFKQINN	YISCFAPGDP	KTLFEYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTAQOE	FREVRLLAIS	VLKNLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ 320
321	RINVVDVSPF	PVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLIG	AISGLASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQOSSTLGNS	VVRCDKLDQS	EIKSLIMCFL	YILKMSDDA	LFTYWNKAST	SELMOFFTIS 480
481	EVCLHQFOYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQQ	LGSLDNSLTF	NHSYGHSDAD	VLHQSLLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLOVI	ISVSQLIADV	VGIGETRPOQ	SLSIINNCAN 720
721	SDRLIKHTSF	SSEVVKDLTKR	IRTVLMTAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDSEMARH	VKNGDLSEAA 800
801	MCYVHVITALV	AEYLTRKGVF	ROGCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIIPYIEKR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRL	KLYSDKFGSE	NVKMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RRFMFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFPYVKK	RIPVMYQHHT	DLNPIEVAID 1040
1041	EMSKKVAELR	QLCSSAEVDM	IKLQKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACQALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPLNSLH	IFNAISGTPT	STMVHGTTSS	SSVV 1194

FIG. 10G (cont.)

	10	20	30	40	50	60	70	80
1	AATTGTAATA	CGACTCACTA	TAGGGCGAAT	TGGGTACCGG	GCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTGATATC
81	GAATTCGGCA	CGAGTTTAC	ACCATCACCA	AAACCCAGAA	TTTTATGATG	AGATTAATAA	AGAGTTGCC	ACTCAGCTGC
161	ATGAAAAGCA	CCACCTGTTG	CTCACATTCT	TCCATGTCAG	CTGTGACAA	TCAAGTAAAG	GAAGCAGGAA	GAAGAGGAT
241	GTGGTTGAAA	CCCAAGTTGG	CTACTCCTGG	CTTCCCTCC	TGAAAGACGG	AAGGGTGGTG	ACAAGCGAGC	AGCACATCCC
321	GGTCTCGGCG	AACCTTCTCT	CGGGCTATCT	TGGCTACCAA	GAGCTTGGGA	TGGGCAGGCA	TTATGGTCCG	GAATTTAAAT
401	GGGTAGATGG	AGGCAAGCCA	CTGCTGAAAA	TTTCCACTCA	TCCTGGTTCT	ACAGGGATAC	TCAGGATCAG	CATTTACATA
481	ATTTTTTCCA	GTACTGTCTAG	AAAACCGAAT	CTGGAGCCCC	AGCCTTAGGA	AACGAACCTG	TAAAGTACCT	TAAGATCTG
561	CATGCGATGG	AAGGCCACGT	GATGATCGCC	TCTTCCCA	CTATCTTAAA	CCAGCTGTTT	CGAGTCTCTA	CCAGAGCCAC
641	ACAGGAAGAA	GTGCGGTTA	ACGTGACTCG	GGTCAATTAT	CATGTGGTTG	CCAGTGCCA	TGAGGAAGGA	TTGGAGAGCC
721	ACTTGAGGTC	ATATGTTAAG	TACGCGTATA	AGGCTGAGCC	ATATGTTGCC	TCTGAATACA	AGACAGTGCA	TGAAGAACT
801	ACCAAAATCCA	TGACCACGAT	TCTCAAGCCT	TCTGCGGATT	TCCTCACCAG	CAACAACTA	CTGAGGTAAT	CATGGTTTTT
881	CTTTGATGTA	CTGATCAAAT	CTATGGCTCA	GCATTGTGTA	GAGAACTCCA	AAGTTAAGTT	GCTGCGAAAC	CAGAGATTTT
961	CTGCATCTTA	TCATCATGCA	GCGGAAACCG	TGTAAATAT	GCTGATGCCA	CACATCACTC	AGAAGTTTGG	AGATAATCCA
1041	GAGGCATCTA	AGAACCGGAA	TCATAGCCTT	GCTGTCTTCA	TCAAGAGATG	TTTCACTTTC	ATGGACAGGG	GCTTTGTCTT
1121	CAAGCAGATC	AACCAACTACA	TTAGCTGTTT	TGCTCTGGA	GACCCAAAGA	CCCTCTTTGA	ATACAAGTTT	GAATTTCTCC
1201	GTGTAGTGTG	CAACCATGAA	CATTATATTC	CGTTGAACTT	ACCAATGCCA	TTTGAAAG	GCAGGATTC	AAGATACCAA
1281	GACCTCCAGC	TTGACTACTC	ATTAAACAGAT	GAGTCTGCA	GAAACCACTT	CTTGGTGGGA	CTGTTACTGA	GGGAGGTGGG
1361	GCAGCGCTTC	CAGGAGTTCC	GGGAGGTCCG	TCTGATCGCC	ATCAGTGTGC	TCAAGAACCT	GCTGATAAAG	CATTCTTTTG
1441	ATGACAGATA	TGCTTCAAGG	AGCCATCAGG	CAAGGATAGC	CACCTCTTAC	CTGCTCTGT	TTGGTCTGCT	GATTGAAAAA
1521	GTCCAGCGGA	TCAATGTGAG	GGATGTGTCA	CCCTTCCCTG	TGAACGCGGG	CATGACCGTG	AAGGATGAAT	CCCTGGCTCT
1601	ACAGCTGTG	AATCCGCTGG	TGACGCGGCA	GAAGGGAAGC	ACCTTGGA	ACAGCCTGCA	CAAGGACCTG	CTGGGCGCCA
1681	TCGCCGCGAT	TGCTTCTCCA	TATACAACCT	CAACTCCAAA	CATCAACAGT	GTGAGAAATG	CTGATTGAG	AGGATCTCTC
1761	ATAAGCAGAG	ATTCCGGTAA	CAGCCTTCCA	GAAAGGAATA	GTGAGAAGAG	CAATTCCCTG	GATAAGCACC	AACAAAGTAG
1841	CACATTGGGA	AATTCCGTGG	TTGCTGTGA	TAACTTGAC	CAGTCTGAGA	TAAAGAGCCT	ACTGATGTGT	TTCTCTTACA
1921	TCITAAAGAG	CATGTCTGAT	GATGCTTTGT	TTACATATTG	GAACAAGGCT	TCAACATCTG	AACCTTATGA	TTTTTTTACA
2001	ATATCTGAAG	TCGCGCTGCA	CCAGTTCAG	TACATGGGGA	AGCGATACAT	AGCCAGGAAC	CAGGAGGGGT	TGGGACCCAT
2081	AGTTCAATGAT	CGAAAGTCTC	AGACATTGCC	TGTTTCCCGT	AACAGAACAG	GAATGATGCA	TGCCAGATTG	CAGCAGCTGG
2161	GCAGCCTGGA	TAACTCTCTC	ACTTTTAAAC	ACAGCTATGG	CCACTCGGAC	GCAGATGTTT	TGCACCAAGT	ATTACTTGAA
2241	GCCAAACATTG	CTACTGAGGT	TTGCCGTGAC	GCTCTGGACA	CGCTTCTCT	ATTTACATTG	GCGTTTAAAG	ACCAGCTCTT
2321	GGCCGACCAT	GGACATAATC	CTCTCATGAA	AAAAGTTTTT	GATGTCTACC	TGTTTCTTCT	TCAAAAACAT	CAGTCTGAAA
2401	CGGCTTTAAA	AAATGTCTTC	ACTTCCCTAA	GGTCCCTAAT	TTATAAGTTT	CCCTCAACAT	TCTATGAAGG	GAGAGCGGAC
2481	ATGTGTGCGG	CTCTGTGTTA	CGAGATTCTC	AAGTCTGTGA	ACTTCAAGCT	GAGCTCCATC	AGGACGGAGG	CTCCAGCT
2561	GCTCTACTTC	CTGATGAGGA	ACAACCTTGA	TTACACTGGA	TTTCAAGTCT	TGTCCGGAC	ACATTGCAA	GTCATCATAT
2641	CTGTGAGCCA	GCTGATAGCA	GACGTTGTG	GCATTGGGGA	AACAGATTAC	CAGCAGTCCC	TGTCCATCAT	CAACAACCTG
2721	GCCAAACGAT	ACCGGCTTAT	TAGCACACCC	AGCTTCTCCT	CTGATGTGAA	GGACTTAAAC	AAAAGGATAC	CAACGGTGCT
2801	AATGGCCACC	GCCACGATGA	AGGAGCATGA	GAACGACCCA	GAGATGCTGG	TGGACCTCCA	GTACAGCCTG	GCCAAATCCT
2881	ATGCCAGCAC	GCCCGAGCTG	AGGAAGACGT	GGCTCGACAG	CATGGCCAGG	ATCCATGTGA	AAAATGGGGA	TCTCTCAGAG
2961	GCAGCAATGT	GCTATGTCCA	CGTAACAGCC	CTAGTGGCAG	AATATCTCAC	ACGGAAAGGC	GTGTTTAGAC	AAGGATGCAC
3041	CGGCTTCAGG	GTCATTACCC	CAAACATGCA	CGAGGAGGCC	TCCATGATGG	AAGACGTGGG	GATGCAGGAT	GTCCATTCTA
3121	ACGAGGATGT	GCTGATGGAG	CTCCTTGAGC	AGTGCGCAGA	TGGACTCTGG	AAAGCCGAGC	GCTACGAGCT	CATGCGCGAC
3201	ATCTACAAAC	TTATCATCCC	CATTTATGAG	AAGCGAGGGG	ATTTCTTTGA	AGATGAAGAT	GGAAAGGAGT	ATATTTACAA
3281	GGAAACCCAA	CTCACACCGC	TGTCCGAAAT	TTCTCAGAGA	CTCCTTAAAC	TGTACTCGGA	TAAATTTGGT	TCTGAAAATG
3361	TCAAAATGAT	ACAGGATTCT	GGCAAGGTCA	ACCCTAAGGA	TCTGGATTCT	AAGTATGCA	ACATCCAGGT	GACTCAGCTC
3441	ATCCCCCTCT	TTGACGAAAA	AGAGTTGCAA	GAAAGGAAAA	CAGAGTTTGA	GAGATCCAC	AACATCCGCC	GCTTCATGTT
3521	TGAGATGCCA	TTTACGCGAG	CCGGGAAGAG	GCAGGGCGGG	GTGGAAGAGC	AGTGCAAAAC	GCGCACCATC	CTGACAGCCA
3601	TACACTGCTT	CCCTTATGTG	AAGAAGCGCA	TCCCTGTCT	GTACCAGCAC	CACACTGACC	TGAACCCCAT	CGAGGTGGCC
3681	ATTGACGAGA	TGAGTAAGAA	GGTGGCGGAG	CTCCGGCAGC	GTGCTCTCTC	GGCCGAGGTG	GACATGATCA	AACTGCAGCT
3761	CAAACTCCAG	GGCAGCGTGA	GGTTTCAGGT	CAATGCTGGC	CCACTAGCAT	ATGCGCGAGC	TTTCTTAGAT	GATACAAACA
3841	CAAAGCGATA	TCTTGACAA	AAAGTGAAGC	TGCTTAAGGA	AGTTTTTCAGG	CAATTTGTGG	AAGCTTGGCG	TCAAGCCTTA
3921	GCGGTAAACG	AACGTCTGAT	TAAAGAAGAC	ATGAGCAGAT	ATCAGGAAGA	AATGAAAGCC	AACTACAGGG	AAATGGCGAA
4001	GGAGCTTTCT	GAAATCATGC	ATGAGCAGAT	CTGCCCCCTG	GAGGAGAAGA	CGAGCGTCTT	ACCGAATCC	CTTCACATCT
4081	TCAACGCCAT	CAGTGGGACT	CCAACAAGCA	CAATGGTTCA	CGGGATGACC	AGCTCGTCTT	CGGTGCTGTG	ATTACATCTC
4161	ATGGCCCGTG	TGTGGGGACT	TGCTTTGTCA	TTTGCAAACT	CAGGATGCTT	TCCAAAGCCA	ATCACTGGGG	AGACCGAGCA
4241	CAGGGAGGAC	CAAGGGGAAG	GGGAGAGAAA	GGAATTAAG	AACAACGTTA	TTTCTTAA	GACTTTCTAT	AGGAGTTGTA
4321	AGAAGGTGCA	CATATTTTTT	TAAATCTCAC	TGGCAATATT	CAAGTTTTC	ATTGTGTCTT	AACAAAGGTG	TGGTAGACAC
4401	TCITGAGCTG	GACTTAGATT	TTATTCTTCC	TTGCAGAGTA	GTGTTAGAA	AGATGGCCTA	CAGAAAAAAA	AGGTTCTGGG
4481	ATCTACATGG	CAGGGAGGGC	TGCACTGACA	TTGATGCTG	GGGGACCTTT	TGCTCGACT	CGTCCGGGAA	ATCTGATCGT
4561	AATCAGGGTA	CAGAACTTAC	TAGTTTTGTC	TAGGAGTATG	TTGTATGACT	AGGATTTGTG	CTATTATCTC	ATTCAACAAC
4641	ATAGAGCAAG	AATAGTGAGC	TAACTGAGCT	AGACACTCAA	TTAATCCGCT	ACTGGCTTCA	AGTCAGAACT	TTGTCAITTA
4721	TCATCGACTC	CGGGACGGTC	ATATATGTAT	TACATTTCTA	CATTTTTAAT	ACTCAATG	GCTTATGCA	TAAGTTTAA
4801	TGTGATAAAT	TTGTGCTGGT	CCAGTATATG	CAATACACTT	TAATGGTTTA	TTCTTGTCT	AAAAATGTGC	AATATGGAGA
4881	TGTATACAAG	TCTTTACT						
	10	20	30	40	50	60	70	80

Fig. 10H

	10	20	30	40	50	60	70	80
1	MEGHVMI	PTILNQLFRV	LTRATQEEVA	VNVTRVVIHV	VAQCHEEGLE	SHLRSYVKYA	YKAEPPYVASE	YKTVHEELTK 80
81	SMTTILKPSA	DFLTSTNKLRL	YSWFFFDVLI	KSMAQHLEIEN	SKVKLLRNQR	FPASYHHAAE	TVVNMIMPHI	TQKFGDNPEA 160
161	SKNANHSLAV	FIKRCFTFMD	RGFVFRQINN	YISCFAPGDP	KTLEFYKFEF	LRVVCNHEHY	IPLNLPMPFG	KGRIQRYQDL 240
241	QLDYSLTDEF	CRNHFLVGLL	LREVGTLAQE	FREVRLIAIS	VLKXLLIKHS	FDDRYASRSH	QARIATLYLP	LPGLLIENVQ 320
321	RINVVDVSPF	FVNAGMTVKD	ESLALPAVNP	LVTPOKGSTL	DNSLHKDLG	AISGIASPYT	TSTPNINSVR	NADSRGSLIS 400
401	TDSGNSLPER	NSEKSNSLDK	HQOSSTLGNS	VVRCDKLDQS	EIKSLLMCFL	YILKMSDDA	LFTYWNKAST	SELMDFFTIS 480
481	EVCLHQFOYM	GKRYIARNQE	GLGPIVHDRK	SQTLPVSRNR	TGMMHARLQ	LGSLENSLTF	NHSYGHSDAD	VLHQSLEAN 560
561	IATEVCLTAL	DTLSLFTLAF	KNQLLADHGH	NPLMKKVFDV	YLCFLQKHQS	ETALKNVFTA	LRSLIYKFPS	TFYEGRADMC 640
641	AALCYEILKC	CNSKLSSIRT	EASQLLYFLM	RNNFDYTGKK	SFVRTHLQVI	ISVSQLIADV	VGIGETRFQQ	SLSIINNCAN 720
721	SDRLIKHTSF	SSDVKDILTKR	IRTVLMATAQ	MKEHENDPEM	LVDLQYSLAK	SYASTPELRK	TWLDSEARH	VINGDLSEAA 800
801	MCYVHVTALV	AEYLTRKGVF	RQCTAFRVI	TPNIDEEASM	MEDVGMQDVH	FNEDVLMELL	EQCADGLWKA	ERYELIADIY 880
881	KLIPIYKRR	RDFFEDEDGK	EYIYKEPKLT	PLSEISQRLI	KLYSDKFGSE	NVRMIQDSGK	VNPKDLDSKY	AYIQVTHVIP 960
961	FFDEKELQER	KTEFERSHNI	RRPFEMPFT	QTGKRQGGVE	EQCKRRTILT	AIHCFFPYVK	RIPVMYQHHT	DLNPIEVAID 1040
1041	EMSKVAELR	QLCSSAEVDM	IKLQKLQGS	VSVQVNAGPL	AYARAFLDDT	NTKRYPDNKV	KLLKEVFRQF	VEACGQALAV 1120
1121	NERLIKEDQL	EYQEEMKANY	REMAKELSEI	MHEQICPLEE	KTSVLPNSLH	IFNAISGTPT	STMVHGMTSS	SSVV 1194

Fig. 10H (cont.)

Exon 1A (-182 to -102)

GCAGGGGAAAAACCTGGCCCCATGATTCACTTACTTCCCACCGGATCTCTCCCATGACACGTGAGGATTA
TTACAATTTAA -102

Exon 1B (-219 to -102)

TTATCCCTTTACTACTTGCGAAGTGAGTTCGGTAGATGGGAGTGGAGAAGAGAACCTTAGAATCATTGTTTAGTCTTCAT
CTTTCACAGCTCAGGCTGAAGGCCTTTCCTTGCTGAGA -102

Exon 1C (-143 to -102)

GCGGCAGAGCGTGTCTGAGGTGGTGCGCGGCTCCGTGCTCCT -102

Exon2 and the rest of human CLASP2 cDNA

-101 -79
GGCAAAGCCAAAGCTAATTGAGC

-78 -1
AAGCTAATTGAGCCACTCGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGTTTACGGGAG

1/1 31/11
ATG CTG CTC TTC CCT TAC GAT GAC TTT CAG ACG GCC ATC CTG AGA CGA CAG GGT CGA TAC
Met leu leu phe pro tyr asp asp phe gln thr ala ile leu arg arg gln gly arg tyr

61/21 91/31
ATA TGC TCA ACA GTG CCT GCG AAG GCG GAA GAG GAA GCA CAG AGC TTG TTT GTT ACA GAG
ile cys ser thr val pro ala lys ala glu glu glu ala gln ser leu phe val thr glu

121/41 151/51
TGC ATC AAA ACC TAT AAC TCT GAC TGG CAT CTT GTG AAC TAT AAA TAT GAA GAT TAC TCA
cys ile lys thr tyr asn ser asp trp his leu val asn tyr lys tyr glu asp tyr ser

181/61 211/71
GGA GAG TTT CGA CAG CTT CCG AAC AAA GTG GTC AAG TTG GAT AAA CTT CCA GTT CAT GTC
gly glu phe arg gln leu pro asn lys val val lys leu asp lys leu pro val his val

241/81 271/91
TAT GAA GTT GAC GAG GAG GTC GAC AAA GAT GAG GAT GCT GCC TCC CTT GGT TCC CAG AAG
tyr glu val asp glu glu val asp lys asp glu asp ala ala ser leu gly ser gln lys

301/101 331/111
GGT GGG ATC ACC AAG CAT GGC TGG CTG TAC AAA GGC AAC ATG AAC AGT GCC ATC AGC GTG
gly gly ile thr lys his gly trp leu tyr lys gly asn met asn ser ala ile ser val

361/121 391/131
ACC ATG AGG TCA TTT AAG AGA CGA TTT TTC CAC CTG ATT CAA CTT GGC GAT GGA TCC TAT
thr met arg ser phe lys arg arg phe phe his leu ile gln leu gly asp gly ser tyr

421/141 451/151
AAT TTG AAT TTT TAT AAA GAT GAA AAG ATC TCC AAA GAA CCA AAA GGA TCA ATA TTT CTG
asn leu asn phe tyr lys asp glu lys ile ser lys glu pro lys gly ser ile phe leu

481/161 511/171
GAT TCC TGT ATG GGT GTC GTT CAG AAC AAC AAA GTC AGG CGT TTT GCT TTT GAG CTC AAG
asp ser cys met gly val val gln asn asn lys val arg arg phe ala phe glu leu lys

541/181	571/191
ATG CAG GAC AAA AGT AGT TAT CTC TTG GCA GCA GAC AGT GAA GTG GAA ATG GAA GAA TGG	
met gln asp lys ser ser tyr leu leu ala ala asp ser glu val glu met glu glu trp	
601/201	631/211
ATC ACA ATT CTA AAT AAG ATC CTC CAG CTC AAC TTT GAA GCT GCA ATG CAA GAA AAG CGA	
ile thr ile leu asn lys ile leu gln leu asn phe glu ala ala met gln glu lys arg	
661/221	691/231
AAT GGC GAC TCT CAC GAA GAT GAT GAA CAA AGC AAA TTG GAA GGT TCT GGT TCC GGT TTA	
asn gly asp ser his glu asp asp glu gln ser lys leu glu gly ser gly ser gly leu	
721/241	751/251
GAT AGC TAC CTG CCG GAA CTT GCC AAG AGT GCA AGA GAA GCA GAA ATC AAA CTA AAA AGT	
asp ser tyr leu pro glu leu ala lys ser ala arg glu ala glu ile lys leu lys ser	
781/261	811/271
GAA AGC AGA GTC AAA CTT TTT TAT TTG GAC CCA GAT GCC CAG AAG CTT GAC TTC TCA TCA	
glu ser arg val lys leu phe tyr leu asp pro asp ala gln lys leu asp phe ser ser	
841/281	871/291
GCT GAG CCA GAA GTG AAG TCA TTT GAA GAG AAG TTT GGA AAA AGG ATC CTT GTC AAG TGC	
ala glu pro glu val lys ser phe glu glu lys phe gly lys arg ile leu val lys cys	
901/301	931/311
AAT GAT TTA TCT TTC AAT TTG CAA TGC TGT GTT GCC GAA AAT GAA GAA GGA CCC ACT ACA	
asn asp leu ser phe asn leu gln cys cys val ala glu asn glu glu gly pro thr thr	
961/321	991/331
AAT GTT GAA CCT TTC TTT GTT ACT CTA TCC CTG TTT GAC ATA AAA TAC AAC CGG AAG ATT	
asn val glu pro phe phe val thr leu ser leu phe asp ile lys tyr asn arg lys ile	
1021/341	1051/351
TCT GCC GAT TTC CAC GTA GAC CTG AAC CAT TTC TCA GTG AGG CAA ATG CTC GCC ACC ACG	
ser ala asp phe his val asp leu asn his phe ser val arg gln met leu ala thr thr	
1081/361	1111/371
TCC CCG GCG CTG ATG AAT GGC AGT GGG CAG AGC CCA TCT GTC CTC AAG GGC ATC CTT CAT	
ser pro ala leu met asn gly ser gly gln ser pro ser val leu lys gly ile leu his	
1141/381	1171/391
GAA GCC GCC ATG CAG TAT CCG AAG CAG GGA ATA TTT TCA GTC ACT TGT CCT CAT CCA GAT	
glu ala ala met gln tyr pro lys gln gly ile phe ser val thr cys pro his pro asp	
1201/401	1231/411
ATA TTT CTT GTG GCC AGA ATT GAA AAA GTC CTT CAG GGG AGC ATC ACA CAT TGC GCT GAG	
ile phe leu val ala arg ile glu lys val leu gln gly ser ile thr his cys ala glu	
1261/421	1291/431
CCA TAT ATG AAA AGT TCA GAC TCT TCT AAG GTG GCC CAG AAG GTG CTG AAG AAT GCC AAG	
pro tyr met lys ser ser asp ser ser lys val ala gln lys val leu lys asn ala lys	
1321/441	1351/451
CAG GCA TGC CAA AGA CTA GGA CAG TAT AGA ATG CCA TTT GCT TGG GCA GCA AGG ACA TTG	
gln ala cys gln arg leu gly gln tyr arg met pro phe ala trp ala ala arg thr leu	

1381/461	1411/471
TTT AAG GAT GCA TCT GGA AAT CTT GAC AAA AAT GCC AGA TTT TCT GCC ATC TAC AGG CAA	
phe lys asp ala ser gly asn leu asp lys asn ala arg phe ser ala ile tyr arg gln	
1441/481	1471/491
GAC AGC AAT AAG CTA TCC AAT GAT GAC ATG CTC AAG TTA CTT GCA GAC TTT CGG AAA CCT	
asp ser asn lys leu ser asn asp asp met leu lys leu leu ala asp phe arg lys pro	
1501/501	1531/511
GAG AAG ATG GCT AAG CTC CCA GTG ATT TTA GGC AAT CTA GAC ATT ACA ATT GAT AAT GTT	
glu lys met ala lys leu pro val ile leu gly asn leu asp ile thr ile asp asn val	
1561/521	1591/531
TCC TCA GAC TTC CCT AAT TAT GTT AAT TCA TCA TAC ATT CCC ACA AAA CAA TTT GAA ACC	
ser ser asp phe pro asn tyr val asn ser ser tyr ile pro thr lys gln phe glu thr	
1621/541	1651/551
TGC AGT AAA ACT CCC ATC ACG TTT GAA GTG GAG GAA TTT GTG CCC TGC ATA CCA AAA CAC	
cys ser lys thr pro ile thr phe glu val glu glu phe val pro cys ile pro lys his	
1681/561	1711/571
ACT CAG CCT TAC ACC ATC TAC ACC AAT CAC CTT TAC GTT TAT CCT AAG TAC TTG AAA TAC	
thr gln pro tyr thr ile tyr thr asn his leu tyr val tyr pro lys tyr leu lys tyr	
1741/581	1771/591
GAC AGT CAG AAG TCT TTT GCC AAG GCT AGA AAT ATT GCG ATT TGC ATT GAA TTC AAA GAT	
asp ser gln lys ser phe ala lys ala arg asn ile ala ile cys ile glu phe lys asp	
1801/601	1831/611
TCA GAT GAG GAA GAC TCT CAG CCC CTT AAG TGC ATT TAT GGC AGA CCT GGT GGG CCA GTT	
ser asp glu glu asp ser gln pro leu lys cys ile tyr gly arg pro gly gly pro val	
1861/621	1891/631
TTC ACA AGA AGC GCC TTT GCT GCA GTT TTA CAC CAT CAC CAA AAC CCA GAA TTT TAT GAT	
phe thr arg ser ala phe ala ala val leu his his his gln asn pro glu phe tyr asp	
1921/641	1951/651
GAG ATT AAA ATA GAG TTG CCC ACT CAG CTG CAT GAA AAG CAC CAC CTG TTG CTC ACA TTC	
glu ile lys ile glu leu pro thr gln leu his glu lys his his leu leu leu thr phe	
1981/661	2011/671
TTC CAT GTC AGC TGT GAC AAC TCA AGT AAA GGA AGC ACG AAG AAG AGG GAT GTC GTT GAA	
phe his val ser cys asp asn ser ser lys gly ser thr lys lys arg asp val val glu	
2041/681	2071/691
ACC CAA GTT GGC TAC TCC TGG CTT CCC CTC CTG AAA GAC GGA AGG GTG GTG ACA AGC GAG	
thr gln val gly tyr ser trp leu pro leu leu lys asp gly arg val val thr ser glu	
2101/701	2131/711
CAG CAC ATC CCG GTC TCG GCG TAC CTT CCT TCG GGC CAT CTT GGC TAC CAA GAG CTT GGG	
gln his ile pro val ser ala tyr leu pro ser gly his leu gly tyr gln glu leu gly	
2161/721	2191/731
ATG GGC AGG CAT TAT GGT CCG GAA ATT AAA TGG GTA GAT GGA GGC AAG CCA CTG CTG AAA	
met gly arg his tyr gly pro glu ile lys trp val asp gly gly lys pro leu leu lys	

2221/741	2251/751
ATT TCC ACT CAT CTG GTT TCT ACA GTG TAT	ACT CAG GAT CAG CAT TTA CAT AAT TTT TTC
ile ser thr his leu val ser thr val tyr	thr gln asp gln his leu his asn phe phe
2281/761	2311/771
CAG TAC TGT CAG AAA ACC GAA TCT GGA GCC	CAA GCC TTA GGA AAC GAA CTT GTA AAG TAC
gln tyr cys gln lys thr glu ser gly ala	gln ala leu gly asn glu leu val lys tyr
2341/781	2371/791
CTT AAG AGT CTG CAT GCG ATG GAA GGC CAC	GTG ATG ATC GCC TTC TTG CCC ACT ATC CTA
leu lys ser leu his ala met glu gly his	val met ile ala phe leu pro thr ile leu
2401/801	2431/811
AAC CAG CTG TTC CGA GTC CTC ACC AGA GCC	ACA CAG GAA GAA GTC GCG GTT AAC GTG ACT
asn gln leu phe arg val leu thr arg ala	thr gln glu glu val ala val asn val thr
2461/821	2491/831
CGG GTC ATT ATT CAT GTG GTT GCC CAG TGC	CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG
arg val ile ile his val val ala gln cys	his glu glu gly leu glu ser his leu arg
2521/841	2551/851
TCA TAT GTT AAG TAC GCG TAT AAG GCT GAG	CCA TAT GTT GCC TCT GAA TAC AAG ACA GTG
ser tyr val lys tyr ala tyr lys ala glu	pro tyr val ala ser glu tyr lys thr val
2581/861	2611/871
CAT GAA GAA CTG ACC AAA TCC ATG ACC ACG	ATT CTC AAG CCT TCT GCC GAT TTC CTC ACC
his glu glu leu thr lys ser met thr thr	ile leu lys pro ser ala asp phe leu thr
2641/881	2671/891
AGC AAC AAA CTA CTG AGG TAC TCA TGG TTT	TTC TTT GAT GTA CTG ATC AAA TCT ATG GCT
ser asn lys leu leu arg tyr ser trp phe	phe phe asp val leu ile lys ser met ala
2701/901	2731/911
CAG CAT TTG ATA GAG AAC TCC AAA GTT AAG	TTG CTG CGA AAC CAG AGA TTT CCT GCA TCC
gln his leu ile glu asn ser lys val lys	leu leu arg asn gln arg phe pro ala ser
2761/921	2791/931
TAT CAT CAT GCA GCG GAA ACC GTT GTA AAT	ATG CTG ATG CCA CAC ATC ACT CAG AAG TTT
tyr his his ala ala glu thr val val asn	met leu met pro his ile thr gln lys phe
2821/941	2851/951
GGA GAT AAT CCA GAG GCA TCT AAG AAC GCG	AAT CAT AGC CTT GCT GTC TTC ATC AAG AGA
gly asp asn pro glu ala ser lys asn ala	asn his ser leu ala val phe ile lys arg
2881/961	2911/971
TGT TTC ACC TTC ATG GAC AGG GGC TTT GTC	TTC AAG CAG ATC AAC AAC TAC ATT AGC TGT
cys phe thr phe met asp arg gly phe val	phe lys gln ile asn asn tyr ile ser cys
2941/981	2971/991
TTT GCT CCT GGA GAC CCA AAG ACC CTC TTT	GAA TAC AAG TTT GAA TTT CTC CGT GTA GTG
phe ala pro gly asp pro lys thr leu phe	glu tyr lys phe glu phe leu arg val val
3001/1001	3031/1011
TGC AAC CAT GAA CAT TAT ATT CCG TTG AAC	TTA CCA ATG CCA TTT GGA AAA GGC AGG ATT
cys asn his glu his tyr ile pro leu asn	leu pro met pro phe gly lys gly arg ile

3061/1021	3091/1031
CAA AGA TAC CAA GAC CTC CAG CTT GAC TAC TCA TTA ACA GAT GAG TTC TGC AGA AAC CAC	gln arg tyr gln asp leu gln leu asp tyr ser leu thr asp glu phe cys arg asn his
3121/1041	3151/1051
TTC TTG GTG GGA CTG TTA CTG AGG GAG GTG GGG ACA GCC CTC CAG GAG TTC CGG GAG GTC	phe leu val gly leu leu leu arg glu val gly thr ala leu gln glu phe arg glu val
3181/1061	3211/1071
CGT CTG ATC GCC ATC AGT GTG CTC AAG AAC CTG CTG ATA AAG CAT TCT TTT GAT GAC AGA	arg leu ile ala ile ser val leu lys asn leu leu ile lys his ser phe asp asp arg
3241/1081	3271/1091
TAT GCT TCA AGG AGC CAT CAG GCA AGG ATA GCC ACC CTC TAC CTG CCT CTG TTT GGT CTG	tyr ala ser arg ser his gln ala arg ile ala thr leu tyr leu pro leu phe gly leu
3301/1101	3331/1111
CTG ATT GAA AAC GTC CAG CGG ATC AAT GTG AGG GAT GTG TCA CCC TTC CCT GTG AAC GCG	leu ile glu asn val gln arg ile asn val arg asp val ser pro phe pro val asn ala
3361/1121	3391/1131
GGC ATG ACC GTG AAG GAT GAA TCC CTG GCT CTA CCA GCT GTG AAT CCG CTG GTG ACG CCG	gly met thr val lys asp glu ser leu ala leu pro ala val asn pro leu val thr pro
3421/1141	3451/1151
CAG AAG GGA AGC ACC CTG GAC AAC AGC CTG CAC AAG GAC CTG CTG GGC GCC ATC TCC GGC	gln lys gly ser thr leu asp asn ser leu his lys asp leu leu gly ala ile ser gly
3481/1161	3511/1171
ATT GCT TCT CCA TAT ACA ACC TCA ACT CCA AAC ATC AAC AGT GTG AGA AAT GCT GAT TCG	ile ala ser pro tyr thr thr ser thr pro asn ile asn ser val arg asn ala asp ser
3541/1181	3571/1191
AGA GGA TCT CTC ATA AGC ACA GAT TCG GGT AAC AGC CTT CCA GAA AGG AAT AGT GAG AAG	arg gly ser leu ile ser thr asp ser gly asn ser leu pro glu arg asn ser glu lys
3601/1201	3631/1211
AGC AAT TCC CTG GAT AAG CAC CAA CAA AGT AGC ACA TTG GGA AAT TCC GTG GTT CGC TGT	ser asn ser leu asp lys his gln gln ser ser thr leu gly asn ser val val arg cys
3661/1221	3691/1231
GAT AAA CTT GAC CAG TCT GAG ATT AAG AGC CTA CTG ATG TGT TTC CTC TAC ATC TTA AAG	asp lys leu asp gln ser glu ile lys ser leu leu met cys phe leu tyr ile leu lys
3721/1241	3751/1251
AGC ATG TCT GAT GAT GCT TTG TTT ACA TAT TGG AAC AAG GCT TCA ACA TCT GAA CTT ATG	ser met ser asp asp ala leu phe thr tyr trp asn lys ala ser thr ser glu leu met
3781/1261	3811/1271
GAT TTT TTT ACA ATA TCT GAA GTC TGC CTG CAC CAG TTC CAG TAC ATG GGG AAG CGA TAC	asp phe phe thr ile ser glu val cys leu his gln phe gln tyr met gly lys arg tyr
3841/1281	3871/1291
ATA GCC AGG AAC CAG GAG GGG TTG GGA CCC ATA GTT CAT GAT CGA AAG TCT CAG ACA TTG	ile ala arg asn gln glu gly leu gly pro ile val his asp arg lys ser gln thr leu

3901/1301	3931/1311
CCT GTT TCC CGT AAC AGA ACA GGA ATG ATG	CAT GCC AGA TTG CAG CAG CTG GGC AGC CTG
pro val ser arg asn arg thr gly met met	his ala arg leu gln gln leu gly ser leu
3961/1321	3991/1331
GAT AAC TCT CTC ACT TTT AAC CAC AGC TAT	GGC CAC TCG GAC GCA GAT GTT CTG CAC CAG
asp asn ser leu thr phe asn his ser tyr	gly his ser asp ala asp val leu his gln
4021/1341	4051/1351
TCA TTA CTT GAA GCC AAC ATT GCT ACT GAG	GTT TGC CTG ACA GCT CTG GAC ACG CTT TCT
ser leu leu glu ala asn ile ala thr glu	val cys leu thr ala leu asp thr leu ser
4081/1361	4111/1371
CTA TTT ACA TTG GCG TTT AAG AAC CAG CTC	CTG GCC GAC CAT GGA CAT AAT CCT CTC ATG
leu phe thr leu ala phe lys asn gln leu	leu ala asp his gly his asn pro leu met
4141/1381	4171/1391
AAA AAA GTT TTT GAT GTC TAC CTG TGT TTT	CTT CAA AAA CAT CAG TCT GAA ACG GCT TTA
lys lys val phe asp val tyr leu cys phe	leu gln lys his gln ser glu thr ala leu
4201/1401	4231/1411
AAA AAT GTC TTC ACT GCC TTA AGG TCC TTA	ATT TAT AAG TTT CCC TCA ACA TTC TAT GAA
lys asn val phe thr ala leu arg ser leu	ile tyr lys phe pro ser thr phe tyr glu
4261/1421	4291/1431
GGG AGA GCG GAC ATG TGT GCG GCT CTG TGT	TAC GAG ATT CTC AAG TGC TGT AAC TCC AAG
gly arg ala asp met cys ala ala leu cys	tyr glu ile leu lys cys cys asn ser lys
4321/1441	4351/1451
CTG AGC TCC ATC AGG ACG GAG GCC TCC CAG	CTG CTC TAC TTC CTG ATG AGG AAC AAC TTT
leu ser ser ile arg thr glu ala ser gln	leu leu tyr phe leu met arg asn asn phe
4381/1461	4411/1471
GAT TAC ACT GGA AAG AAG TCC TTT GTC CGG	ACA CAT TTG CAA GTC ATC ATA TCT GTC AGC
asp tyr thr gly lys lys ser phe val arg	thr his leu gln val ile ile ser val ser
4441/1481	4471/1491
CAG CTG ATA GCA GAC GTT GTT GGC ATT GGG	GAA ACC AGA TTC CAG CAG TCC CTG TCC ATC
gln leu ile ala asp val val gly ile gly	glu thr arg phe gln gln ser leu ser ile
4501/1501	4531/1511
ATC AAC AAC TGT GCC AAC AGT GAC CGG CTT	ATT AAG CAC ACC AGC TTC TCC TCT GAT GTG
ile asn asn cys ala asn ser asp arg leu	ile lys his thr ser phe ser ser asp val
4561/1521	4591/1531
AAG GAC TTA ACC AAA AGG ATA CGC ACG GTG	CTA ATG GCC ACC GCC CAG ATG AAG GAG CAT
lys asp leu thr lys arg ile arg thr val	leu met ala thr ala gln met lys glu his
4621/1541	4651/1551
GAG AAC GAC CCA GAG ATG CTG GTG GAC CTC	CAG TAC AGC CTG GCC AAA TCC TAT GCC AGC
glu asn asp pro glu met leu val asp leu	gln tyr ser leu ala lys ser tyr ala ser
4681/1561	4711/1571
ACG CCC GAG CTC AGG AAG ACG TGG CTC GAC	AGC ATG GCC AGG ATC CAT GTC AAA AAT GGC
thr pro glu leu arg lys thr trp leu asp	ser met ala arg ile his val lys asn gly

4741/1581	4771/1591
GAT CTC TCA GAG GCA GCA ATG TGC TAT GTC CAC GTA ACA GCC CTA GTG GCA GAA TAT CTC	
asp leu ser glu ala ala met cys tyr val his val thr ala leu val ala glu tyr leu	
4801/1601	4831/1611
ACA CGG AAA GGC GTG TTT AGA CAA GGA TGC ACC GCC TTC AGG GTC ATT ACC CCA AAC ATC	
thr arg lys gly val phe arg gln gly cys thr ala phe arg val ile thr pro asn ile	
4861/1621	4891/1631
GAC GAG GAG GCC TCC ATG ATG GAA GAC GTG GGG ATG CAG GAT GTC CAT TTC AAC GAG GAT	
asp glu glu ala ser met met glu asp val gly met gln asp val his phe asn glu asp	
4921/1641	4951/1651
GTG CTG ATG GAG CTC CTT GAG CAG TGC GCA GAT GGA CTC TGG AAA GCC GAG CGC TAC GAG	
val leu met glu leu leu glu gln cys ala asp gly leu trp lys ala glu arg tyr glu	
4981/1661	5011/1671
CTC ATC GCC GAC ATC TAC AAA CTT ATC ATC CCC ATT TAT GAG AAG CGG AGG GAT TTC TTT	
leu ile ala asp ile tyr lys leu ile ile pro ile tyr glu lys arg arg asp phe phe	
5041/1681	5071/1691
GAA GAT GAA GAT GGA AAG GAG TAT ATT TAC AAG GAA CCC AAA CTC ACA CCG CTG TCG GAA	
glu asp glu asp gly lys glu tyr ile tyr lys glu pro lys leu thr pro leu ser glu	
5101/1701	5131/1711
ATT TCT CAG AGA CTC CTT AAA CTG TAC TCG GAT AAA TTT GGT TCT GAA AAT GTC AAA ATG	
ile ser gln arg leu leu lys leu tyr ser asp lys phe gly ser glu asn val lys met	
5161/1721	5191/1731
ATA CAG GAT TCT GGC AAG GTC AAC CCT AAG GAT CTG GAT TCT AAG TAT GCA TAC ATC CAG	
ile gln asp ser gly lys val asn pro lys asp leu asp ser lys tyr ala tyr ile gln	
5221/1741	5251/1751
GTG ACT CAC GTC ATC CCC TTC TTT GAC GAA AAA GAG TTG CAA GAA AGG AAA ACA GAG TTT	
val thr his val ile pro phe phe asp glu lys glu leu gln glu arg lys thr glu phe	
5281/1761	5311/1771
GAG AGA TCC CAC AAC ATC CGC CGC TTC ATG TTT GAG ATG CCA TTT ACG CAG ACC GGG AAG	
glu arg ser his asn ile arg arg phe met phe glu met pro phe thr gln thr gly lys	
5341/1781	5371/1791
AGG CAG GGC GGG GTG GAA GAG CAG TGC AAA CGG CGC ACC ATC CTG ACA GCC ATA CAC TGC	
arg gln gly gly val glu glu gln cys lys arg arg thr ile leu thr ala ile his cys	
5401/1801	5431/1811
TTC CCT TAT GTG AAG AAG CGC ATC CCT GTC ATG TAC CAG CAC CAC ACT GAC CTG AAC CCC	
phe pro tyr val lys lys arg ile pro val met tyr gln his his thr asp leu asn pro	
5461/1821	5491/1831
ATC GAG GTG GCC ATT GAC GAG ATG AGT AAG AAG GTG GCG GAG CTC CGG CAG CTG TGC TCC	
ile glu val ala ile asp glu met ser lys lys val ala glu leu arg gln leu cys ser	
5521/1841	5551/1851
TCG GCC GAG GTG GAC ATG ATC AAA CTG CAG CTC AAA CTC CAG GGC AGC GTG AGT GTT CAG	
ser ala glu val asp met ile lys leu gln leu lys leu gln gly ser val ser val gln	

5581/1861	5611/1871
GTC AAT GCT GGC CCA CTA GCA TAT GCG CGA	GCT TTC TTA GAT GAT ACA AAC ACA AAG CGA
val asn ala gly pro leu ala tyr ala arg	ala phe leu asp asp thr asn thr lys arg
5641/1881	5671/1891
TAT CCT GAC AAT AAA GTG AAG CTG CTT AAG	GAA GTT TTC AGG CAA TTT GTG GAA GCT TGC
tyr pro asp asn lys val lys leu leu lys	glu val phe arg gln phe val glu ala cys
5701/1901	5731/1911
GGT CAA GCC TTA GCG GTA AAC GAA CGT CTG	ATT AAA GAA GAC CAG CTC GAG TAT CAG GAA
gly gln ala leu ala val asn glu arg leu	ile lys glu asp gln leu glu tyr gln glu
5761/1921	5791/1931
GAA ATG AAA GCC AAC TAC AGG GAA ATG GCG	AAG GAG CTT TCT GAA ATC ATG CAT GAG CAG
glu met lys ala asn tyr arg glu met ala	lys glu leu ser glu ile met his glu gln
5821/1941	5851/1951
ATC TGC CCC CTG GAG GAG AAG ACG AGC GTC	TTA CCG AAT TCC CTT CAC ATC TTC AAC GCC
ile cys pro leu glu glu lys thr ser val	leu pro asn ser leu his ile phe asn ala
5881/1961	5911/1971
ATC AGT GGG ACT CCA ACA AGC ACA ATG GTT	CAC GGG ATG ACC AGC TCG TCT TCG GTC GTG
ile ser gly thr pro thr ser thr met val	his gly met thr ser ser ser ser val val
5941/1981	5971
TGA TTA CAT CTC ATG GCC CGT GTG TGG GGA	CTT GCT TTG TCA TTT GCA AAC TCA GGA TGC
6001	6031
TTT CCA AAG CCA ATC ACT GGG GAG ACC GAG	CAC AGG GAG GAC CAA GGG GAA GGG GAG AGA
6061	6091
AAG GAA ATA AAG AAC AAC GTT ATT-TCT TAA	CAG ACT TTC TAT AGG AGT TGT AAG AAG GTG
6121	6151
CAC ATA TTT TTT TAA ATC TCA CTG GCA ATA	TTC AAA GTT TTC ATT GTG TCT TAA CAA AGG
6181	6211
TGT GGT AGA CAC TCT TGA GCT GGA CTT AGA	TTT TAT TCT TCC TTG CAG AGT AGT GTT AGA
6241	6271
ATA GAT GGC CTA CAG AAA AAA AAG GTT CTG	GGA TCT ACA TGG CAG GGA GGG CTG CAC TGA
6301	6331
CAT TGA TGC CTG GGG GAC CTT TTG CCT CGA	CTC GTG CCG GAA ATC TGA TCG TAA TCA GGG
6361	6391
TAC AGA ACT TAC TAG TTT TGT CTA GGA GTA	TGT TGT ATG ACT AGG ATT TGT GCT ATT ATC
6421	6451
TCA TTC AAC AAC ATA GAG CAA GAA TAG TGA	GCT AAC TGA GCT AGA CAC TCA ATT AAT CCG
6481	6511
CTA CTG GCT TCA AGT CAG AAC TTT GTC ATT	AAT CAT CGA CTC CGG GAC GGT CAT ATA TGT
6541	6571
ATT ACA TTT CTA CAT TTT TAA TAC TCA CAT	GGG CTT ATG CAT TAA GTT TAA TTG TGA TAA
6601	6631
ATT TGT GCT GGT CCA GTA TAT GCA ATA CAC	TTT AAT GGT TTA TTC TTG TCA TAA AAA TGT
6661	
GCA ATA TGG AGA TGT ATA CAA GTC TTT ACT	

A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-2 cDNA isoforms

Isoform	Difference	Nucleotide(s)	Consequence
1	polymorphism	862	A to G change; mis-sense mutation
2	polymorphism		A to C change; mis-sense mutation changing codon from histidine to proline
3	polymorphism	2210	A to G change; mis-sense mutation changing codon from asparagine to glutamic acid
4	polymorphism	2225	C to T change; mis-sense mutation changing codon from histidine to tyrosine

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	209-291	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein

These differences may be found separately or together in various combinations in the different human CLASP-2 isoforms

FIG. 11B

human CLASP-2

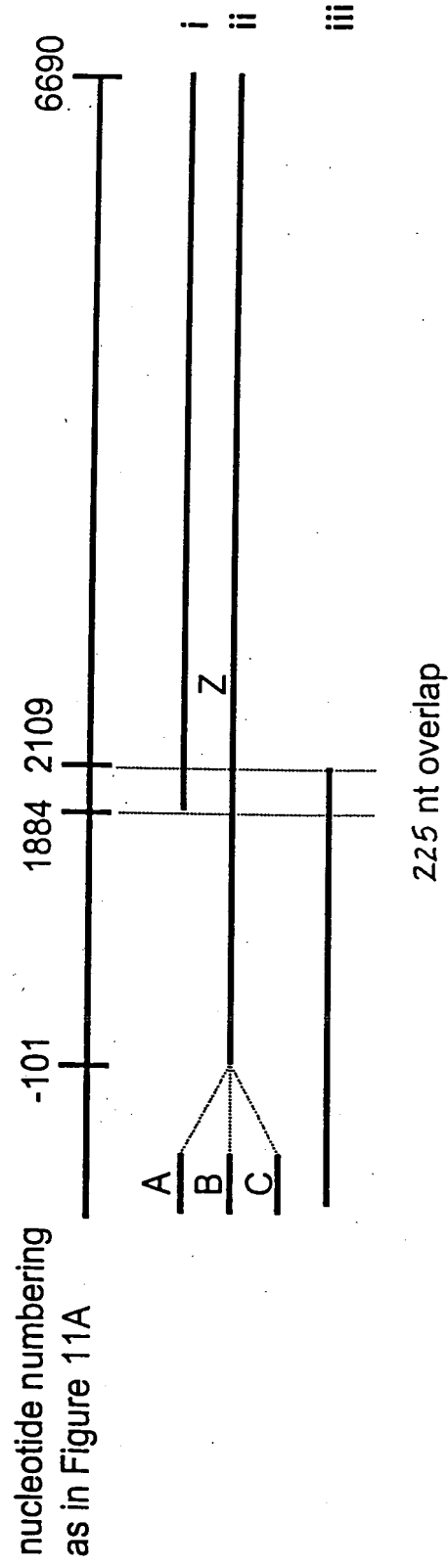


FIG. 11C

1st exon (nucleotides 335 to 445)

TGTCTTGCTTATCTTTTCGCCCTCCAGGCAAAGCCAAAGCTAATTGAGCCACT
CGACTATGAAAATGTCATCGTCCAGAAGAAGACTCAGATCCTGAACGACTGT
TTACGGGAGATGCTGCTCTTCCCTTACGATGACTTTCAGGTAAGTAACGTTAT
GTTTCTATCCGTAGAACCACG

2nd exon (nucleotides 7101-7190)

TTACCCAAGGCTTTTCCTCCTGTTTTTGTTCAGACGGCCATCCTGAGACGA
CAGGGTCGATACATATGCTCAACAGTGCCTGCGAAGGCGGAAGAGGAAGCA
CAGAGCTTGTTTGTTACAGAGGTAAGGCTCTTTCCTGCATTAATTTACATTTT
GAAGTCATTTTCCCCTAACTGCCTCC

3rd exon (nucleotides 11439 to 11521)

TTTTCTATTTTTTAAAATCCCCCTTCAATAGTGCATCAAAACCTATAACTCTGAC
TGGCATCTTGTTGAACATAAATATGAAGATTACTCAGGAGAGTTTCGACAGC
TTCCGAAGTGAGTAAGCTATATTATACACATAGGGAAAAGTCTTT

4th exon (nucleotides 13987 to 14056)

CTAAAACAAATTTTCTTTGTTGTTTTATAGCAAAGTGGTCAAGTTGGATAAA
CTTCCAGTTTCATGTCTATGAAGTTGACGAGGAGGTCGACAAAGATGAGGTGG
GATACCTGCTTGCTGTTGCTTCTCTTTTCACTCTAGATTAA

5th exon (nucleotides 15212 to 15307)

GGAGGTTGACTGCTGGTGTTCCTTCTCTCCTAGGATGCTGCCTCCCTTGGT
CCCAGAAGGGTGGGATCACCAAGCATGGCTGGCTGTACAAAGGCAACATGA
ACAGTGCCATCAGCGTGACCATGAGGGTGAGGACGCACATCACTTTGCCCTC
CCCTCTCACAAAGCCCTTC

6th exon (nucleotides 16269 to 16404)

TGAAAGAATAGCTGTGTGTATATTTTTCTCTCAGTCATTTAAGAGACGATTTT
TCCACCTGATTCAACTTGGCGATGGATCCTATAATTTGAATTTTTATAAAGAT
GAAAAGATCTCCAAAGAACCAAAAGGATCAATATTTCTGGATTCTGTATGG
GTGTCGTTTCAAGTAAATATGAAAAGAGTTTTACCATTATGTTTTCTTA

7th exon (nucleotides 19459 to 19633)

AAGTATGTCTGTTTATCCTTTTTTCATTTTCAGAACAAACAAAGTCAGGCGTTTT
GCTTTTGAGCTCAAGATGCAGGACAAAAGTAGTTATCTCTTGGCAGCAGACA
GTGAAGTGGAAATGGAAGAATGGATCACAATTCTAAATAAGATCCTCCAGCT
CAACTTTGAAGCTGCAATGCAAGAAAAGCGAAATGGCGACTCTCACGAAGGT
AGATAGGCTTGGCTTCCCCCAGGCACATACACACTCT

8th exon (nucleotides 20567 to 20634)

ATTACAAGTGATTCCGATAATCTGTTTTGCCATTTTAGATGATGAACAAAGCA
AATTGGAAGGTTCTGGTTCCGGTTTAGATAGCTACCTGCCGGAAGTTGCCAAG
GTAACATCGTCTTATATCTTCTGCTCTTCGTTGAATGC

9th exon (nucleotides 30257 to 30331)

GATTGTGTAAATGTAATTTTCATGTATCTTGTTATCAGAGTGCAAGAGAAGC
AGAAATCAAACATAAAAAGTGAAAGCAGAGTCAAACCTTTTTTATTTGGACCCA
GATGCCCAGGTAAGAACTATCTAAATGTTTAATATTTAAAACCAAAT

10th exon (nucleotides 31851 to 31991)

CATAACTTATTTATATGTTTACATTTTCTTTTAAAGAAGCTTGACTTCTCATCA
GCTGAGCCAGAAAGTGAAGTCATTTGAAGAGAAGTTTGGAAAAAGGATCCTTG
TCAAGTGCAATGATTTATCTTTCAATTTGCAATGCTGTGTTGCCGAAAATGAA
GAAGGACCCACTACAAATGTAATTTTTCATTTTAAAAATAAACATTAAAAAA
AAAATAGGCAG

11th exon (nucleotides 32472 to 32675)

CCATGGTGATCATTGGATTGTTTTGTTTTGTTTCAGGTTGAACCTTTCTTTGTTA
CTCTATCCCTGTTTGACATAAAATACAACCGGAAGATTTCTGCCGATTTCCAC
GTAGACCTGAACCATTTCTCAGTGAGGCAAATGCTCGCCACCACGTCCCCGG
CGCTGATGAATGGCAGTGGGCAGAGCCCATCTGTCCTCAAGGGCATCCTTCA
TGAAGCCGCCATGCAGTATCCGAAGCAGGTGGGGAGTATGAGCCCAGCATTC
CCACTACTCAGACTCACTTTGCATGC

12th exon (nucleotides 33063 to 33185)

GAATTCTGCTTACTGAAGAAAATTGTTTGCCTCCTAGGGAATATTTTCAGTCA
CTTGTCTCATCCAGATATATTTCTTGTGGCCAGAATTGAAAAAGTCCTTCAG
GGGAGCATCACACATTGCGCTGAGCCATATATGAAAAGTTCAGACTCTTCTA
AGGTATGAATGGCTTTTACGCTTTGGGGTGGTAAAAAGCAATCTGAA

13th exon (nucleotides 36702 to 36784)

CAGTATCTCATAGCTTTATTCTCATGTCTTCAAGGTGGCCCAGAAGGTGCTGA
AGAATGCCAAGCAGGCATGCCAAAGACTAGGACAGTATAGAATGCCATTTGC
TTGGGCAGCAAGGTAAGGAACACCTTTTATACCTTTTAAATCGATATAGATA
GGTGCATGG

14th partial exon (nucleotides 37353 to 37475)

GAAACCCAGTTTAGAAATGTTGCTTTGCCATTTTCAGGACATTGTTTAAAGGATG
CATCTGGAAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGA
CAGCAATAAGCTATCCAATGATGACATGCTCAAGTTACTTGCAGACTTTTCGG
AA

1 TACCAAGGGCAACTCTGGCACACCCCTAAAGTCTGGAAGGGGACATAGCTAGTCAGGGATGACCCGAGAAATGACTGGAAGCTCCACCAGAA
93 TGCAGAGCTTCCTTTGTGCTTAAATAACTGAACAAGCATCACTCTGTGTAGCAGGACACCACCAGCATTTTTTGTCCCTTTGGAAACAAC
185 CTTATTTCTGTTTTCTTTGTGATACCAAACTAGCATACTCTAATTGTAGAAAATACAAAACATAGAGTAGAACATACTAAGTTCTTTATCTT
277 AAGAAATGGCATTTGTGTATGAGAATGCTTTGCTTATCTTTTCGCCCTCCAGGCAAAGCCAAAGCTAATTGAGCCACTCGACTATGAAAATG
369 TCATCGTCCAGAAGAACTCAGATCCTGAACGACTGTTTACGGGAGATGCTGCTCTTCCCTTACGATGACTTTAGGTAAGTAACGTTATG
461 TTTCTATCCGTAGAACACGTTGATCTTAACAAGCAGTATTTTCTATGTATTGATTATTGTTTGGTTAGTTAATTATTATTATTATT
553 ATTTTTTTTGTAGACACAGTCTTGCTCTGTACGCAGGCTTGAGTGCAGTGGTGCCATCTTGGCTCAACGGCAACCTCCGCCCTCTGGGTCA
645 AGCATTTCTCTGCCCTCAGCCTCTCAAGTAACGTTGATTACAGGCGTGTGCCACCATGCTTGGCTAAATTTTGTCTTTGTATTAGAGACAGG
737 GTTTTGGCCACGGTGGCCAGGGTCGTCCCAAACCTCTGGCCTTAAGTGATCTATCTGCCCTTGGCCTCTCAAAATGTTGGGATTATAGGCATGA
829 GCCACTGTGCCCCGCCCTAATTATGGTTTTTAAAGATGAAAATAAGATGTTATTTAAGAAAGAAAAGTTATTTTATATTCTTCCAAGCATCC
921 TTCATGAGTTGATAATTTTAAATGGTATTATTTTGCATATTAAATTATAAGTATGCCAAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGT
1013 GTGTATCTTGAATAAAAGTGCTATACTCTGTCTGGGCTGATTTAGTGGGCACAAGTGCCCTTCTGTCTTTTGTAGATTTGTTTTGATTTAGAT
1105 TTTTGTGGCCAGTACCTTAGAATCTTAATGATGGCTTTGTCTGGGAGCAGTGGGAGATTTCGTATGCCTTTTTTTAGGATGGCATTGGG
1197 AGCCTGCCTTCAAGGCCCCTGCACTCTGTGTGGGCTCCAGCAAAGCGTTCAAGGTTAGCCAAGAATGCCCTGAAGTTTACCTCTGTAGTGT
1289 AATGTGGGTGCTGTTCCTTGAAGAAATGTGGAGGACTCAGCACAGCTCCTGCTGTGTGCCGCTCTTTCAGGCTATGGCCTGTGGTTAAGAG
1381 ACTAACAAGAAGCTGTGAGGCTGTTGAGGAATGAGAATGACATTCTTCCTCCAGGAAACCCGGTGGTGTAAATGCCTTGACGCGAGCCACC
1473 TTGGTCCATTTGGAGGTTCTGGTTACTTTCTTGTCTTCCTGGGACCTGATCTGGCACCTCTTTCTCTCTCCTTTGATGCTCTTAGTTGG
1565 ACACCTTCTCTACCTGATGCTGTATACCATTTAAGCCCTGTCTTTTGTGAATCGAGCTGCCCTTTTTTTTAAAGCTTCACTGATCTTTGTGT
1657 TTGATTCCAAAAGTGTACATCCATGTACAAAAGATAAATGAGAGGGAAATATTGAAATAATTGACATGAAAAGCCTCCCCACGCCCTTCTA
1749 ATCCCATCCACAGAACATGACTTAACGTATACAGCTCTGTGCATACTTGTCTTTAGAACTTCCATGTTAATAGAAATTGTAAATTACG
1841 ATCCTTGAAGGTTTTTTCCACCAAATTTAAGCGACTCCAGCTTACAACAGAGGTGAGAATTTACAAATGTTCACTCTTTCTAACTTGT
1933 AGAGATACCTGGGCCCCAAAATGATTATCTTTAGCTCTGTCTGCATAAAAGGAATGCCCATGGGAATGAAATGACCATTCTGTGTGGTGT
2025 TGCTACCAAAGTAACAGGTAAATGGGTTGAGGTCATGCCAAACAATACCATGCTTTGCATACTTCATTTGATGACTAACTGCATGGGAACG
2117 GACTAATAAATGAGAACCTCTGAATGATGCCTTTTGCCTGTGATTTGGCAACAATGAAAAGCAAATCAAATGATTATAAAATGTACTGCA
2209 TGTTGACAAGATTTTCTGTAGTGTGTCTGAGGAAGCTAAAGGTTATCTCAAATTTCTCTCAACATGAAGTATGTGTTCTTCTTGGTATTA
2301 ATTAAAGTAACAACTTTTTTGAGTTTGCAACCTAGAATGAAAAATCTATTGTATGACTGAGATAAAATGCTTAAAGAAACAACCAAAGAA
2393 ACGAGATACAGTTAGTTGAGTGTCTTTATCCAGGGAACAGGTATCTGGATGTTTAAAGCAGTTGCAGAATCAGACAGTTTAAACTTTGA
2485 GAAAACCTCTGTGTCCCTTTTGTCTTTAACTACTCTGGTGATAGCAGGCACAAATATTCTAGGAAAGGCAAAGAACTCACTAGCATTGTT
2577 GGCTAAGGTGATGAGCAAATATTATTTCTGTTTGGGGAGAAGTTTTCCTAGAGATTAGGAGCTTGAATTGGAGCTTTAATCTCATCACA
2669 GGAATTGTGATGGGCCCCAGTGAAGTTGGGTACAATTATTTGTTTTCTTATAGACTCCCACTTTCTTATCAGGTAAGCCATGTACTCTGT
2761 GCTTTCTTGTAAATGTCTCAGTGATGTTATTAAGTGTCTAATTAGCTGGATGAGTGAAAGGTCTTAACAGTGCCACAGATTCTTCTATC
2853 TGTGTTTTCTTAGGCAGAATAAGAGCAGAATTATTGTATTATTAGAGGCAGAGGGAACAAATTAGATTGGGGAAAGTGTTTATTTCATATG
2945 GAAAAGTAATAACCAAGTTGGTTAGGAAATGGCAGCAGCAAAACGCATGCTGAGGGGTGATTTACTGCACTTAAATAATTAGCAGTATAAGT
3037 TAACTATTAAATAATAGAACTTGGTGTCCATTTCTGCCAAATATATTGAAATGACAATTTACTAAATATAAGCATGGATAGTGGTGATG
3129 CTGTGTACATTTTCAAGTAGGCACATGTTGATCTTGAGCCTTTACTGGTCAGATCCTAAAGGCATCTACATGTTCTCTAAAAATGAGTTG
3221 TGTCAAGAAAAGATTTGCGGGTTGCATGTAGTTGCCCTGAGGATGACAGAAGAGTAGTTACTACAACAGCAGCAAGAAGAGAGACATGAAGT
3313 AAACGTGGATTTTAAAAATCAAAGAATAGGCCAGGCGCACTGGCTCATGCTGTAATCCAGCACCTTTGGGAGGCCGAGGTGGGCAGATC
3405 ACAAGGTCAGGAGTTTGAGACCAGCCTGGCCAATATGGTGAAACCCCATCTCTACCAGAAAATACAAAATTAGCCAGGCATGGTGGTGCATG
3497 CCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGATCTCTTGAAACAGGAGACAGAGGTTGCAGTAAGCTGAGATCGTCCACTGCA
3589 TTCCAGCCTGGGCGACAGAGTGAGACTCATCTCAAAACAAACAAAATCAAATAATAGTTCCAGCCATCAGGTTATTGATGAAGTAGG
3681 CTGGGCACGGTGGCTCACACCTGTAATCCAGCACATTGGGAGTCCGAGGCAGGTGGATCACCTGAGGTCAGGTGTTTGTAGACCAGCCTGGC
3773 CAACATGGCAAAACCCGCTCTTACTAAAAATACAAAATTAGCCAGGCATGGTGGTGGGCACCTATAATCCCAGCTACTTGGGAGGCTGAG
3865 GCAAGAGAATCGCTTGAACCTGGGAGGTGGAGGTGCAAGTGTGAGCAAGATCGCGCCATTGCACTCCAGCCTGGGGGACAAGAGGAAAACCTC
3957 ATCTCAAAAAAAAAAAGGAATATTAAATGAAGTAAAGTACATGTGATCTGCCATGGCCAGGGACAGGAATGCCATGGGGCCTGCAGCCGTCA
4049 CTAGCTGATGGCCCTCTTTTTTGCAGAATCAGATCCTGTGCTTGGGGATCTCTGCCATCTGTGCTTTGGCTTCATGGTTCTCTTGGCAGC
4141 AGCATCTTCTCTTCTAGATCTTTCTACCCCTTTAGAGACCCTTGAATCCCATATTGTCTGAAGCTATTTAAGTCCACAGAACTTTTCCC
4233 CCCACTGTCTCAATTCTTTCTTACTGCCTGTCTGCACCGTGCACATAAACACTTGAGTATGTGGTCTTGGCTGTTCACGACCTACTTCTTA
4325 GGCTTCTTGACCGCAGGCATCCGCCCCGTGTGTGGTCTTGAGAAGGCTGGCTTTGAGCCTCTGTTCTCCACCCACCTGCCACCTACA
4417 CATGCACAAAATCCCTTTCTTGCTAGGTGCTAGGGTTGAATACCCATTGCTTACCTTACTAATAGTAAATTTTACAAGCATTAGGTTATT
4509 TTCTTTGATTCATCAAGTAAATATTAACTGTTTGAACATGTGATAGTCCAGCGACTAGATTGTAAAAATATTGACAGGATCAATGAT

4601 TTGGTTTGGCAGAAGTAGGTAATTTCTAAAATTAAAAATGCAGGTAAAACAGGGACTGGAGAGGAGTATTTTTTCTAGTGATTAATAAAC
4693 CTTTATTTTTCTTATTGTTTTGTGTCTTACCCAGTTTATTTGGCGTAAATCTGAGAACCTTACTTTTTCCATGAGCAAAGTTAGAGGTA AAC
4785 TTTAAACAAGCAGTTAGACAGAGGTAATGACCTTTAGATTAAAAGGTTTTAGGTCAGCTGTATAAGTTGACTTGTGCTTAAGACATGATGA
4877 GCCTCTGTTTAACTGAAAGTCAAGCCCAGGACGCCTGCCTTTTCCATCAAAGACATGGGATTGGGTGGCAGCTGACTATTGATTTCCAATG
4969 ACGATTCTTCTTCAAGTGGAGGTCCTTTTACCAGATGGTCTGTGGTGGGACATTGTTAACCTGCGATTAAACCGACGGCATCTTCATCT
5061 GGC'TTTAAGCTCCTTGTATCCTGACTTGTACACAGCTTACTTATGCTTGTGCGACTATGTAAAGTGACAGTATATGAGAAAGGTAGTGAG
5153 TAGTAAGAATGTTGGGAGACAATTTAAGCTACCATTTCATATTTTCATAAAAAATTAGACTTTTGTGTCTGGTGTAAACAAACAGAGGACAGAGC
5245 TTGTATGAAAGGATAAAAGAGCGTTAAGGGTTACACGTCATTAGGATAAAAAAACTAGAATATTCTTTCTGAAACCTGAAGCCCAGGCCG
5337 GGCATGGTGGCTCACGCCCTGTAATCTCAGCACCTTTGGGAGGTTGAGATGGGAGATTGTTTGGAGCCAGGAGTTTGGAGCCAGCCTGGGCAAC
5429 ATGGTGAAACCCCATCTCTATTAAAGAATAAGGCTGGGTGTGGTGGCTCACACCTGTAATCCTAGTGCTTTGGGAGTGTGAGGCAGGTGGA
5521 TTGCTTGAGTTGAGGAGTTTGGAGCCAGCTTGGGCAACATGGTGAACCCCATCTGTACTAAAAATACAAAAATTAGGCGGGTGTGGTGGCG
5613 CCCGCTGTAGTCCAGCTACTCAGGAGGCTGAAGCATGACAATCACTTGAACCTGGGAGGCAGAGGTTGAGTGAGCCGAGATCATGCCAC
5705 TGCATCCAGCCTGGGTGACAGAGAGAGACTCCGTCTCAAAAAATTAAAAAATTAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCAGCA
5797 CTTTGGGAGGCCGAGGTGGGAGATCACGAGGTGAGGAGATTGAGACCATCTGGCTAACACGGTGAACCCCGTCTCTACTAAAAATACAA
5889 AAAATTAGTTGGGCATGGTGGCAGGCCCTGTAGTCCAGCTGCTCGGGAGGCTGAGGCAGAAGATGGCGTGAACCCGGGAGGCGGAGCTG
5981 GCAGTGAGCTGAGATTGCCCACTGCACTCCAGACTGGGCGACAGAGCGAGACCTGTCTCAAAAAATAAAATAAAATAAAATAAAATAA
6073 ATTAAGAAAGAAAAGAAAAGGAAACCTTAAGCCTAGTTATTGAGGTAGACAGGATGCTACCCCTGCCCTGTCTTTTATTAAAGAGCAT
6165 TTAAGCCTAATGAACACGAGCAGTTCTAATGTCCGTTGGAGGGGAGGTAGCATTACAGTTTATAGATTGATTGAGC
6257 ATCTTCTGTGTCTAGTTATCTATGCTCTTAGGCGCTGGGATGTGGCAGTGAACAAGAAGAGATGTAAATGACAAGAGATGGATGGTGGT
6349 GATGGTTGCACAATTGTGTGAATGTACTTAATGCCACTGAACTGTATACTTAAAAATGTTCAAAATGGCTGGGCATGGTGGCTCACGCCTGT
6441 AATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACCTGAGATTAGGAGTTCGAGACCAGCCTGATCAACATGGAGAAACCCGCTCTA
6533 CTAAAAATACAAAAATAACCGAGCGTGGTGGCGCATGCCCTGTAATCCAGCTACTCGGGAGGCTGAGACAGGAGAATCGCTTGAACCCGGGT
6625 GGCGGAGGTTGAGTGAGCCGAGATCCCGCCATTGCACTCCAGCCTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAAGTTTCAAATGG
6717 TAAATTTATGCATATTTTACCAGAATAAAAAAAGGCAGTTAAGACAAGTAAGATGCTGTGTGTCATGGGGCTAGATCAAGCACTTAGGGGTGGG
6809 GTGTTAGGGACTTTGAACGGGGCCTCTACCCTGCGGGAAGGGCTGAGCTGGAGGGATCTGTGGGCCCCGATCAAGAAAGAGCAGGAGCTG
6901 TAACCCAGCCTGGCTTTGGAACCTGAGGCTGCCAGTGAATCTGTTGTGTGTGACGGAAGGAGGAGCCTGCACTGGATGGGAGAACTGGA
6993 GGGACTCTGTGGCTGCCAGGGCCAGCTGCAGGGCACAGCTGCACTCTGAGGCTGGCACCTGCCCTCTTCACTTACCCAAGGCTTTTCCTC
7085 CTGTTTTTGTTCAGACGGCCATCTGAGACGACAGGGTCGATACATATGCTCAACAGTGCCCTGGAAGGCGGAAGAGGAAGCACAGAGCT
7177 TGTGTTGTACAGAGGTAAGGCTCTTCTGCAATTAATTTACATTTTGAAGTCATTTTCCCTAACGCTCTCTTTCTTTAAATTTCAAAT
7269 TGTCAAGGAAGTGTCAAAGGGTAATTGTATTTCTATGATGGAAGTTCAAATAGAATAATGTGAATTTTTCAGACTCTGAACTTGGACAGA
7361 AATGTCCACAGGGGCTATTTCTTTTACATTTTATTATTTTAAACTTTATTTATTTGGAGGGGCTATATCTGACTACAAAAAGTGAA
7453 TTCCACAGAATTTATCTCATGGACTTAAATAAGCAGTAACCTTGAAATGAATTCAGTGGAAATCTGTGGGAGGCTTGTATTGATACTGT
7545 TTTTAAGGGTGACACACATTTATGTATCATTTATTTTATTTATATATATTTGATTACTATATATATTTCTAATCAAGATACATTGATTAAT
7637 GCTGATAATAAGCAGGGTCTATCGCTAGTCAATATATATTTATATATATTTGATTACTATATATATTTCTAATCAAGATACATTGATTAAT
7729 ATTATTTTGTGTTGAAAATGCAAATAAAATTATCTTATGGAAGAAAGATAAATATTTTACTTTTTTATTTTATTTTATTTTGTAGACAG
7821 AGTCTTGCTCTGTTGTCTAAGCTAGAGTGCTGTGGAGCAATCTTGGCTCACTGCAACCTCTGCCTCTCTGGGTCAAGTGGTCTCTCTGCC
7913 TCAGCCTCCCAAGTAGCTGGGATTACAGGCGTGACCCACGCGCTGGCTAACCTTTGTATTTTATAGTAGGACAGGGTTTCAGCCTGTTAG
8005 TCAGGCTGGTCTCAGACTCCTGACCTCAAGTGATCTGCCCGCTTGGCCTCCCAAAGTGCTAGGATTACTGGCATGAGCCACTGTGCCTGGC
8097 CAGAAAGAGAAATTATTACAATTTAGGTTGTTTGTCTTTAGTTTTTCCCTTGGAGTGTTGTTTTTCTCCAGGTAATTTTAGGTAGGAAG
8189 GAATAATTAGATGTTTAAATTTGTTTCTTTAAGTGACCTTCATTTAAAAATAATGATTTTTTTTAAATCCTGGTTTTTCTAGTTGATATT
8281 TAGATCATAAATATGCTCATCAATAAAATTGCTTACTATAAGGAAGCTATAAATACTCTTATAAAGACCAATTAATAACAATATTTAATTT
8373 CCATTGAGATTTTTGAAAAATTAAATATAAAATTAAAAAATTTTAAGTGTGTCCCTCATCTTTCTGAAGAAGTAACCTCTGTCTTACCT
8465 CCTTTGCCACTATATTAGTAACTTAATCCAGACAAATACAGCCAGATATGTTTGTGAATGTAGTTATAAATGTCTTTTTAAGGCAGGTAG
8557 TGGCAAACATGACCTGCAAGCAAATCCAGCCTGTAGCCAATTTTGTAAATAAAGTTTATTGTAAAGCAGCCAAGCACATTTGTTTACA
8649 TATTGCCATATGGCTACTGTCAACATGCAACTCAAAGTTAAGTAGAGATAATATGACCTCAAAGCTGAAAATATTTATGATCTGCGCTTTTA
8741 CACAAAAAGTTTGTGACCTATGTTTTAAAGCATGTGGCAAAATTTAATTTGCTAACTCAGTTCTCCAGTTGATTAAAAAATATGGTTT
8833 TTTGAGGGAGAACTCTCCATTAGTTATTTAATCACTGCAGGTTGAGCAATAGCTGCTTCATCCTATGCTGCTGGAGCCAACATAACTAAAC
8925 ACTTTTGGGACCTTCCACTTGGGTGGAGTGAACATCACTTCTCTTCATCTCTGATCCAGGGAATGACCTAATGGCTTAAAAACAAAGCAA
9017 AACAAAGCAGAAAAAACTTCAAAAACCTTTCAGTGTAACCTTCAAAATATTATTGAATTTACCAGTTTGAAATGTTAATCGTATAATCAGT
9109 CAGTCACATTCTCTGCTTTTTGAAGGTACAGTTCTCAGGATCTGGCTTCTGATGGAACCTTATCTCCTAGACTTTCTGCATCCCCAGAG

FIG. 12B
2 of 10

13801 ACTCAAGTCTCTTGGCTTACCCACCTTGAAAAGCAAGGGCATAGATGGTTTTATTCTTTGTCTGAATAAAGAAGCTGGGCCATCTTTGGATT
13893 TAGTAAAGGCCGGGCCCTATGATGGAGGAAGAAATGCAAAGCCTCTTCCTTGACTAGGCATTCTAAAACAAATTTCTTTGTGTTTTAT
13985 AGCAAAGTGGTCAAGTTGGATAAACTTCCAGTTCATGTCTATGAAGTTGACGAGGAGGTCGACAAAGATGAGGTGGGATACCTGCTTGCTGT
14077 TGCTTCTCTTTTCACTCTAGATTTAAACATCAATTTTACAGACTTAGAAGATTAGTTAGAAAATTACCGACATTTAGCCAAAACAGGCATTG
14169 GAGTGTACATGAAACGGGAATAATTTTAAAAATGTTATTGATTGATTGGAATAAGGTCTCTGTTTCAACTTTACTGCTTAGCATTTTCAT
14261 GTTCTCTTGGTTGTGTTTATTTGTTCTGAGATCATTTTCAAAGACTTGGATCAGATCTGGCTACATTGTTAAAAGATATCAAGATGACTTAG
14353 ACCTTGAATTTAGGTTGTTTTTCAACAGATCTCGAAACAGCTGCCAGCCAGTAGATTTAAATGGCTATTCTTCAATGATTGCTTTTAGTGA
14445 AGTCTGATTGATCAAGCCCACTCCCCCTATTCTTAGAGGAAAGCTCATGGCTAAAGAACTATATAAGGGAGTAGGGCATTGAGATGAGTC
14537 TGCCCACTGAGTGAGGGAACCTCACAGAAGACAATGCCCATCTCTGCATTTCTCATCTCCCCATTGATTGTTAAGTGTCCTATTGTGAG
14629 TTTAGGTTTTCTCTTCTTAAAAAAATGTGAGCTGAGCTATAACATTAGCCACTCATTAAAGCAATGTGCATGTAGCAAATTATTTTATTCT
14721 CCCCCATCACTTTATCTCTCTCTTCTGTATTGCTTCAATTTCTCTCCCTTGCTTTATTACCTTTCTCTGAACCTCTGGGAAGGTTTC
14813 CAGGAATGTGCATGTGCTTTTGTCTCTGACTATAGGGGAGTGTCATTGAAAACATTTTTCGTGAACACAGGCAAGACCTTCCAACGTGA
14905 GTGGTCAGTTGAGGTATGCTCTTTTGGTCTCTTTGTGGCTCATTAAACACTGACAAATAAAAAATTTGGACAGGAGCTAGCTTTGCCCTTAA
14997 TGAATAAAGTTTTTCAAGAAATGTAGGCGGGTCTCTCTTTTCAACCGCTAAGTGGACTTTTATGTGACTTGTAGGCATTGGTGTCAATGGGTG
15089 CTTCAAGTAAAGGGCAATGGACAACCTTGGCACAAAGGGAATGACCTTCCCATTGACCAAACCTCACAGCAAGCAACCCAGGTAATAACGGGAG
15181 GTTGACTGCTGGTGTCTTCTCTCTCTAGGATGCTGCCCTCCCTTGGTTCCAGAGGGTGGGATCACCAGCATGGCTGGCTGTACAAAG
15273 GCAACATGAACAGTGCCATCAGCGTGACCATGAGGGTGAGGACGCACATCACTTTGCCCTCCCTCTCACAGCCCTTTCTGCCATAGAGCT
15365 CGAGAACAATGCTCAAGATGAATGCGCATGCTGTTCTTCCCAACAAAAGGGACATTGTCTGATTCTTAGGATGCTCCCTGGTGATAGCACC
15457 CCCATTGGCACAGCCTCATCCACCCACTTTCCCTCACTGTCTTCTGACCACCAGCATAAGGAGACCATCCCTGGGCTGGTGTGAAGGTGCAG
15549 ACACTGACATAGGCTTTCTCTCTGTAATAACTGAAAAGTGCTCTTTGGTACCTCACAGAATGTACCAAGGGGCTATCTGTCTATGCCAATC
15641 CTGAGCACTTCTGTGGAGGTGACTGCAGCAAAGTCAAGTAAAGCAAAAATTGAGGACGAGAAAAGAAAATAGTTGCATAGAAGAGAAGGTT
15733 GCAGACAGAGAAGTCAAAACATAGAAGAAGCTATTGAGGAGAAAAGTGGGACCAGAGGAACATCAGGATTAAATAACAAAGGGAAGAGAAAC
15825 AAGGGAGTCAGGGAGATAAAAAATTAAGGAGGAAATGTGACTGTCATTACCTTAAGGCTGGAATAATCATTACGCGTCATGAGGCAAAAAATAG
15917 TTCCCATCTGTGAGCAAGAAACCCTGGGGATTTTAGAGAAAGTTCTGTCTTCTGTGCTGCATCCCAAATGGAAGTCCCTGCACTGCTT
16009 TTGGGTAGTTATGTAAAATCTCTGATTCCGTGGGTGAGAAAATGACCCATGGATATTAGGGGAACCACTCTCAGAACTGAGATGCAGTG
16101 AGCTTCTTAGATGGGATGGGAGTCTTGACCCACAGTGACCTGGAGCATCAGCTAGAGTGAGAACGGAACAGGTTTTATGTATGTATGTA
16193 GTCATAAGTGGGTATTGATAGAGATTGTGACCTCTTCATTTTGAAAGAATAGCTGTGTATATTTTCTCTCAGTCATTAAAGAGACGA
16285 TTTTTCACCTGATTCAACTTGGCGATGGATCTATAATTTGAATTTTATAAAGATGAAAAGATCTCCAAAGAACAAAAGGATCAATATT
16377 TCTGGATTCTGTATGGGTGTCGTTCAAGTAAATATGAAAAGAGTTTTTACCATTATGTTTTCTTATCTGCAGTAGTGCCTATGTGTAAATTA
16469 GCAGATTTAAGCAAACACTTCCAAAATGGCAATATGCATGGTAGAAATATAACATATAACTTTAAATGAGGCAAGCCTGTGTTTTTCATCAT
16561 TGTAGAAGATGGAAGGGATAATGTAGAGGCAGAAATATGCTGTGGCAGGCAGGAGCACTCTGGCTCGGCCACTTTATAGCTGCGTGACCTTT
16653 AACAGGCTACTTAATTCAGATAATGAGAATGTTCTTTAATACGGCAATGAGTACATTGGATGAATCAGTGCAAGGAAATATTTAAACAC
16745 TTCATAGTATCTCAGTGGTGATTTTTATCGTAGCATTGTAGTAGCAGTGCGGTGTAGATCAGTAAAGAGATTAGGTTTCAGCGCAGATTG
16837 AGTTCAAATCCCTGCTCCTCCACTTACCAACTGTGTAACCTTGGAGATGTTATTTAACCCTCTCTGTACCTCAGTTTCTTCATTTGTTAAATA
16929 AGGATAATGGCAGTACCAAAATATGGTTACTGAGAGGGTTCATTATTACACATGTAAAAAGCTTAGAACAGTGCCAAACAAATGGTAAGCATT
17021 TGGTCAGTATTAGATAGTTTTGTATCATAGGGCTGTGTACTTTTATATCATAGGGCTTATGTACTTATCCTTTAAATTTATTGTTAATTA
17113 AAGATAACACATGAATGTATTTTCTTGTAAAAAATCAGCCAATACAGATAAAGTGAAAGTCCTTCTGGACTCTCCCTCCTTCAGTGCTCT
17205 CTTTTCTGAGGGGAGCTACTACCAGTTTTGCATGCATCCTTCTGTAGCTTTTTCAGATTGTCTTTGGAAGAGAGTTGTCAATTTCCCTGTCC
17297 ATCATCTGTCCATCCATCCATCCATCCATCTGTCCACCCCTCCATTTCATCCAGCCTTGCCACTTTCAAGGAAGATTAAAGGCAGCAGC
17389 TTATAAGCATACACAGGACATGGGATAGCATAAATTTAAAGTGGGGTGAAAGCAGAAAGATGAACAGGGGATTGGGATAAGGGTGAGAGAA
17481 AATAGAGTTAAGGAGAAAGCGTATGTTTTGAAGATCTAACACCTGCTGTGGGTGGGCCACCACCTGGGCTCTATGCTTTCTCACTTGGAGAC
17573 CTGTTTAGTCACGCAATTACAGTGACATGAGATAAAGGCATGATGCTGTAGTCTAGTCTAGAACACCCCTGACTTTAAAAAGAAGT
17665 TAAAGCAAAACTAAATGTATTTGGCAACCTCATTTTTTAAAGTAGGAAGTAATTATTTTGTGTTTATAAGAGAGTTTGTGCTGCTGTTCTG
17757 GCCCAGGGACAGATGTTTATAAGTACAACCTGCCCTGAGCTATCAATTAGTCTCCGGGTGCATTTCAAATCTAAGGTTCTGACTTCAATGG
17849 AAGTCTCTTCTTCAAATGTCTTTGAGATGCAGCTGATGGTGTTCATTTAATAAAGTGTATCCAAGGCTTCAAAAAAGTAAAAAATTT
17941 TGTTTTTATCTGTGCTGTTTGTAAACTAAGCATCAAAAGTTGTGATTAAAGTGTGTTTTAAAAATTTACTTATGGATATTATAAAAAAT
18033 TAGTTGACTGGTGCTGTGAATAAAAAAGTGCCATAAACTAAAAAATTTGAAGCATTTTAGAACCTTGAAATTTATTATACTTATTTTGC
18125 AGATGAGAAAAGTGAAGCTCAGAAACAGAAATTTAGAATTGAGGCCTAATGTTTTTCTCCACTTTTAACTTTCTTTTCATGATTGTGA
18217 GTATGAGGAAAGGAGGAGAGAAATTCATTTTGTTCAGCCCTTGACTTCTCCCTGGTCTTGGCTTGAAGTTAAGTGAATCCAAA
18309 GTGGCAATTACTGAGCCACAGCAGACAGTCTGTGCACAAGAGTGTGTGGCTTTGCCAAGGGGAGCACTTGACTTTGCATTTCTAAGAAGT

FIG. 12B
4 of 10

18401 TGCTGCAGAATCACAGAGACTTTTGGGAGGGTGGCCCTGTCCCTGAGACCTCCACCAAGGAACCTCTTAGAGAGAGTGTGGATAACCCAGTAG
18493 GATTTTAGTGGCTATGCGGGGGGCTGTCCTGCTGGCTCAGGTTAGTGGGAGTGTGATTTCATATCGCTCAGCCTGTCCCTACAGGGGATC
18585 TTGTGCCATGATCCTCAGAGCTGAACCTCTGTCTACTGCGGCCAACCTGGGGAGATTTTGCTCCCTGGAGGACATCTTGAATGTCTGAAGA
18677 CTGGCATCTATTGGCTTAAGGCCATAAATTCGCTAAACATTGTACAATGCATGGACCAGCCACTCACAACAAAGAATTGGCTGCCCAAGTG
18769 TCAGTAGTACCGAGATTGAGAAATCCTGGCCTAGTGCATGTTTCATCTTCCGTCTGTTACTGCACATGGACTACTGTTCTTGTCTGTGAGCC
18861 AGTCACCTCTTTCAGGCATGAAAACCTGGAGGCATGAGGCAAGGCCACGGACAGGGAGTCCAAATACCTTTTGGGATTTCATAAAGGATGGGA
18953 AAGTTCAGATAAGTAAGCCAAACATAGTAATAGATAATGGTTGGCTTTTAAAAATGTAATACCATACACTACTTCATTAAAAAATAGGAG
19045 CTGAAGAAATATGAAAATTTTACATGAAATTCATTTATTCACAAATATTTTCAAATACCCACTATGTGCAAGTCACCTGTAGAGTCCATA
19137 GAGACTAAGGATGTGTAGCACTGACAAAAATGGGAGCACTGAGGAGGTTTCATTCCACTGCAGGGACACACAGTGAATCAGATGAGTATGTA
19229 AAGCAGGTAATGAGTCAGAAGGAAAAATAAGCTTGCAGAAAGTGAAGCAGGGAAGGTGGACGGTAATGGGATTTCATGGGGGGGGGCTTTC
19321 ATGAGGAGGGGGCAAGCTATTTAAAAATAGCTTGGTTCTAAATGCCAATGAGATATCACTACCAACAAGAGAGAGTAATTATTTTAAAGCAG
19413 TTCTAATTCCTTTTAAAGTATGTCTGTTTATCCTTTTTTCATTTTCAGAACAAAGAGTCAGGCGTTTTGCTTTTGAGCTCAAGATGCAGGACA
19505 AAAGTAGTTATCTCTTGGCAGCAGACAGTGAAGTGGAAATGGAAGAATGGATCACAATCTAAATAAGATCCTCCAGCTCAACTTTGAAGCT
19597 GCAATGCAAGAAAAGCGAAATGGCGACTCTCAGGAAGTAGATAGGCTTGGCTTCCCCAGGCACATACACACTCTGTGGGTGTCTTTATTT
19689 TTGCCAGGTGGGTATAAGAAGGAGACCTGTGTTACACAAGTACATGAGAGGTGGGACGGATAGGAGCTCTTTACAAATATCCTGTACGAAA
19781 GGTTTTGTACATTATAACTTACTTCCCTGACATTTCTGATATGGAATCATGTAATGGGAAGAACCAAGCTTTGGAGGCAGAAAGGGAGA
19873 CCTGGGTTTGAGTGCATATAAATACTGTATTTAGCTGTGTAGCCCTGGGTAAACAACCTTATGTTTTCTGAGCCTCAGTTGACTCACCTATAA
19965 AATGGGAATAAACATGAAAATTTGCTGGGAAGTGGGAAGTGAATAAGAAAATGAATCTCAAGTATCTGGCATAGAATTTTACTGTATTAT
20057 AAAATATTAGTAATAATTAGAATGCATGGGAGCCTCAGATTAAATTTGGTGAGAAAAATCTGGCTATGTTCTTGACAATTCATGTTTTACTTC
20149 AACCTTAGGTGATTCCCAACCTTGGCTTCCCTTAGAAGTACCTGGGAGCTTTTTAAAAATACCATTACCTGGTCCCAAAAAGATTCTG
20241 ATTTAGTTGGTCTGGGTGGAGCTGGGACGGTCTGACTTTTAGGGGTCTCATGGACGTGTCCATGTGGGCTGTTGTTTCATAGCTAGTGTG
20333 AGTTCTAATTGGACGGTGTCCATGCTATACCAGCTGCTCAGTGTGTTGACTTTCATCACTGAGCCTGTGGATCAGTATTTTTTCAAAGCAC
20425 CCAAGTGTTCAGGAGCATCCAGAGTGGGAACCACTGTGTTTCAATTTGAAGGCACCTAAGAGAAACGGCTTCTCTCTCTGTTTCAAAT
20517 GAAATGCTATGAATTACAAGTGATTCGATAATCTGTTTTGCCATTTTAGATGATGAACAAAGCAAATGGAAGGTTCTGGTTCCGGTTTAG
20609 ATAGCTACCTGCCGGAACCTGCCAAGGTAACATCGTCTTATATCTTCTGCTCTTCTGTTGAATGCTGTTGAAGTATGTCTCATTTCACTGGTT
20701 TGTCCAGAATGGAATCTGTTGAAATCATAAAAATTACATTGTGATTACCTCTCTCTTTTTCTGACCTGATTACGAGGTGACGTGTACTCATG
20793 CAGTATGATTTTAGGTTCTGTCTTCTAAAAAGTACCCTACAAAGCATCTCTCTTTTATTATTATTTTAAAGTGTTTTTTCCCTGATAATGCTT
20885 AACACTGCATCAGGTAAGTACTGAAGAAATAACTGAAATATGCAGGCAGATGTTCTATAATAGCATCGTACTTTCTATGTTGATACATGTGCT
20977 CTCCTTACTCAGGTAATAGACACGGTTCCAAAGAGGAAGACCTGGTAATCTGCCACGAAACCCGGGGGTGCTGAGTTACAGAAATT
21069 GTTTCGGGTCACTCTTACTGGAAAAAAATAAGCTATTCTGTGCTTACAATTTTGAGAAATTTAAAGTTACTGAAAGCACAAAGAAAA
21161 GCAAATCAACCATACTGCTACTTCCAGATTAAATATCTATTATGATGTTGCCCTTTTAGCTTCCATATTCTTAAAGATATAAACATCGG
21253 TTATAGTTGAAGTCTTTTTAAACACTGTCTTATTCCCATCTCTTCTCTCCACAAACCCCAATCAGAAACAAGCACTATTTAAAGTTTT
21345 ACTTTCAATTTTATATCTTTACAAATAAATCTATCATAATGATATATACAGTATGATTTAGTATGTTTAAAAATGTTTATAAATGCTAACA
21437 TACCATATGATTCTGCACCTTAAAAAATTTTAAATTTACCCCTTTTATTGTTACTATATAGACTTTTTATTGTTAGCTGTCTATTATTTT
21529 CATTTTTTCTATTATAAACAAAGCTACAAAGTACTGTCTTGTACTTGTGCTTGTGTGATCTGAATGATCTTTCTTAAATGAGAGAAA
21621 TATCTTTGTCTTCTAGCCCTTTGCACTCTTACTCTGTACTGCCCTTCTATTCTTTTTGATACTAGAGTGAAATGGCGACCTCCACAC
21713 CCACATCTTAAACACTATAATAGAAACATGGTTTATCTATATAGGATTATAAATAGACCAGCATTGACGATTGACCTTTATTTAAGACAAC
21805 ATGGCTGTTCTCAAGTGTAATCTCCCTCCCTGGCTAGGGCTTTAGAGCAATGTTTTTCTTTAGGACTTGACTGCTACCACAGTATCTTTT
21897 TAGCACCTGCCTATTAAAGCTAATTTTAGTGCCACCATTGTAACCACCTCCTAGTCTGGGAAGAGTTTTGGCTTGTGTGTTGTGTTATGA
21989 ATGCTGTGTATCATATTTTGCATTGAGATTGCTTTTTTGTGTTCTGGATGTTTGGGGGTTTCATAATTTCTCAAAACAAAATATTTGTGCCC
22081 ATTTGGGTTTATGTTTGTGTCAGCAGGTAATATATGTGATGCCATCTAGAATTCAGAAAGTAACCTTCTGCACTTACTGGGTGAACCGGAATG
22173 GATACCTAGGAGAAGATTTCATGTTATTTGAGCCTAATGTTGATTAAATTAATAATCTATGCTTTTTCCCTATGAGGATATACAGGAACGGTCCC
22265 CTCCTTCTCTTACTACCCAGCCAATATAATTCAGTATTGTTGATCCCAAGACCTAGGGAGATTTTTTAAGATATACATATATTTAATATAA
22357 ATGTATACATTTATGTATATATACTTTTTTATAAGTATAATTGTATATTTTGTCAATTTAAATATTTTGAAGTATTTTAAACTATGGGTTA
22449 CAAGTTAGGTTAAGCCATTTTAGTTGGTGAATCAGTTTGATTTCAACCCCTGCTTCTTTTTGTTTTGTTTCTATTAGTTTTTTATTCTTT
22541 TTATTGAGGTATAATTTGCAATAGCAGAATGCTCAACATGAATTGTAGAGCTCACTGGAGTTCGCATTGTACACTGATATAAGCAGCCCT
22633 CAGGCTAGCTTGTACCTGAGACCTCTTTATTTGACCTCCATCACCCTAGATTAGTTTTGACTTTTCTAGACCTTCTGTGAATGGACTTA
22725 TACATGTACTCTTTGTGTGAGGCTTATTTAGCTAAACATGTGATTCACCTTTAAGAAGTTTTTTTTAGGTGGGCATAGTGGCTCATGCCGTG
22817 AATCCAGCACTTTGGGAGGCTGAGGTGAGCGGATCTTTTGGGTTAGGAGTTCAAGACCAGCCTTGCCAACATGGTATAAAACCTGTCTC
22909 TACTAGAAATACAAAAATTAGCTAGGCGTGGTGGCAGGTGCCTGTAATCCAGCTACTTTGGGAGGCTGAGGCAGGAGAATCATTTGACCTG

23001 GAAGGCAGAGATTGCAGTGAGCTGAGATCATGCCACTGCACTCTAGCCTGGGTGACAGAGCAAGACTGTGTCTCAAAAAAAAAAAGGGTC
 23093 CGTTTTAATGAAATAAAATGGAATGGAGAATATGAAAGTACACTGCCCTTAATAATGACATTATTTTTTATATAAAATACTGTCATTATTAT
 23185 TTTGGTGGCACCTGCCACCATGCCAGCTAGCTAATTTTGTATTCTAGTAGAGACAGGGTTTATACCATGTTGGCGAGGCTGGTCTTGAACTC
 23277 CTAACCTCAAAAGATCCACCCACCTCAGCCTCCCAAAGTGCTGAGATTACAGGCATGAGCCACTACGCCCACCTGAAAAAAAAACTTTTTAA
 23369 AGTGAATTACATAATTTTTTACATAAAATAATGTCATTATTAAGGGCAATGTACTATTTATACATATAGTGTGTATGTGTCTTGCATAGT
 23461 GATATAAAAGATATTTGTTTTCTTAGTGTGCTATTATGTATATTTATTTACTTTCATTGGTATATAATGTACCTATTTTGGGAGTTCATGT
 23553 GATACTTTGATATCTGTATACAATGTGTGATGATCAAATCAGGATAATTTGGGATAGCCATCACCTCAAACATTTATCTTTGTGTTGGGAATT
 23645 TGAAACATTTCTTACCAGGAGTCATGGTCAAACCTGAAAAATGAATCCTTGTAGAGGCTTTTACTCTTCCCCCTGGCTTTCAGGTGTTT
 23737 TACAAATACTTTTATTTAGGAAGGTAGAAAGGTGAAAGTAATTTTGAAGGGGAAAAGAATGAAGAAAATGGAGATGAGTTATTCACCTCA
 23829 GCACATGGGTATCTGTGGGCTTTGCCCTTTAAAGCCAGCTTGGTGTGAGTGTGAGCAGCCAGGCAGTAAGGGGAGACCTGTGTTCCCAT
 23921 CCCCAGCCTTGAGCAAAAATGCAGTTTGGCTGTTTATCATCCCCCTTCAGGGTGTCTGAACTATTTGCACCGGTTGAGAAGGCAAAGAAGT
 24013 TGACCTGATAACTGTTGGTCATCCATTAGGAAGGATGGATTTCATGGTTACAGAATCAGAGACTGAAGTATGCAGAGGGAGGGGTGGGGAG
 24105 AGAGAACTGTGCAAGGAGTTTACCAGGGTATGAAGAGGTAAAGAGGTCAGTATCAGGGAAGGAAGGTGCAAGAAAGGGTCAGGCTGGGAGG
 24197 CTGGGCCACAGTTCAGTAAGATTACAAAGAAGGGCTAGAACAAATGAGGGCAGGCAGAGGTTGGCTGAAGGTGTAATTTTCATGGCAGGTCC
 24289 TTTTCTAATCAGCTCCTCTAACCTCCTTCATCTGTTGCCCGGGCTTTGTTTTCCACTGTGACTAAGACATAGCCAAACAGGATATGACCG
 24381 ACAGGAAGTTGTTTCAGTGCAAAAATAACTGATGTCCTATTCTGGAATATTATGAAGGGCTCATTACTTACAGTGTGAGTGATGTAACCC
 24473 AGGTTTTAGAAATATTTTGTATAATCTTGAGCTTATGTTTGTACATTTAGTACTGAACATCTGTATTGTTTTCTTATTAGAGAACACACTG
 24565 TATTTACCTTAAACTGGTTCCTTTCTCTATTGTCTATTATGGAACCAACAATTTTTATTGTAATGTAACAGTGTGTAGCATCAGTCT
 24657 TATAAATATTTTAGTTGATACACAACCGTAGTTCAGTTAGTTAATGATTCTTCCCTAGAAAGTCAAGGAGTAACATAATCAGGTTAT
 24749 AAACCTCATTACTAGTTATTTAATAATTTATTTCTCTGGTTACATTTATATCTTAGGTGACATCAGAACATATATGTCACCTCCTTAAAGAT
 24841 AGTGTGAAGAAAACCCACCTTATGTTTTCTCCACAGCTTTTCTGTTTGTGAGCTTTTATTTTGTACTCAAAGAATAGCATCCAACCTTTTA
 24933 CTTTGGTTTCCCATGTGGTCTGAAAGAGAAGTAGAATTTCTTAAATCCGGAATTGCTCACATCCTTTACCTTTAACTTTGTTTTAA
 25025 GCAATGAACCTTATTGTTCCAGGTAATCTTCCACAGTTGCATGCAGGGGAAAGTATGATGTCTCAGACTTTATAGTCTCATGGAGATGGAG
 25117 TGAGGATCAAGGGCCATGCTCAGCAGAACTTGTGAGGCCAGCAGTTTCACGGACACCTTTTCTTAATTTTAAACCAAGTCTATAATAAG
 25209 TGCTTTCTTCCCTAGATTCCAATCCAGAAAACATATCATTGCACTATTATACAAAGGAGCTGGCTAGGCTTGTGTCTGTGGGGTCAGCTGG
 25301 TGTGTCATTTCTGGGCCCTCTTTGTGAAGAGGATGAACGATGGTCTGAGAAGTTAGGTGTCTTGAAGTAGTGGAAATAAATCATGATAA
 25393 CTCTTTAAATTAAAGATTATATATTTTGGCCTCAAAACATTTTGCAAAGTCTCTCTATTCCAACCCAATCTGTTTAAATGACCCAACATTCA
 25485 ACACATTGTTTCTGATAATTCTCCTCAGAATAAGATGCTGTTGGCCATAATCTTTGTCTCTAGATTGTTTTATCTACTCGCAATAAATTT
 25577 AAGACACAGAGTATGCCATAAGCCTACAGCAGACTTTCTGGAAACTCTTGAATGTTTGGTCCATAACTACTTCTTAAGACAAAGAAGAAAC
 25669 CTTGTGAGGGTGTGTCTTAGTGCTTGAATGTAGGGTTTACAGGATGGGGTGGGGGGAATCGCCCTTGGTTTAGATGAATCATTCTTT
 25761 TCCTTGTCTTCTCAGCAACACCAGTTTCTACAGAGAACAGCTCTGCCATTGTGCATTTTCTGTCTCCATTTTCTCTCATTCCTCTCCA
 25853 CGAAACCCAGAGTAGTCAGTGGGCTTTGGGCAGGAAAGTGGAACAGGGTGTCTGGGAAAAGCCAGTTGGCTCTTCTTACCATCACAAATAT
 25945 AGACTGACCACAGGTTATTTAAGAGCAGAGCTGGTTTCCATCACTCTGAGAAGTGTCAACTACAGACTTTGGGATGATATTTGTTATAGC
 26037 TGTATTTTCTCCACTCTTAGATTGTGAAAGTACATATTACAAGTATTTATTTTATTATCTTTACTAAAATTTTAATTAAGAAAGAGCGTGCT
 26129 TGCCGCAATAAGTAAAAATACCCAAAGTTGTTTAAAGAAAAGTTACCTTTTCCCTTCATCTCCATTCCACATTCTTGAGAACACTGAAG
 26221 TTAATAACCGGTTGCAATTTCCCTTTTACCACAACTGATTGCTCATAGAAATATAGATAAACATATGTAAGGTTTTTAAGTTTTTTAATAAA
 26313 AATATGTTTCATGATATATACATTATTCTGAAATTTTCTGTATCACTTAAAAATATTTTCATAGATGTCCCTCTGGGCCAGTGGAAGATCTGGT
 26405 TCCCCCTTACATACATATCAGCAAGCTGCATGATATTTCAACTATTGCTACTGCACAGTTTATTTCAGCCATCTCCCTATTATGAACATTTA
 26497 AGGTTTTTTTTTTCAGTTTTTGTAGCTCTACAAACAGTACACAATAAACAACATGACATTAAATACTTGTGCTCTTATTTTCAGTAGGAGAAAT
 26589 CCCCATGTGGAATTTTTAAGTCAAAGTTTATTGTGTTTTTAAATGCTTTAAACATTGCCAGGTTACCGTCCCAAAAGGCTATAACAATTCAC
 26681 ATTTCTGTTTCTCTGCATCTTACCAGACGAGTGTAAGATGGTATTTTACTGTGCTTTCATTTATATTTTGTGTTTATTAGTGATATTTTT
 26773 CATATTTTCATATATTTATTTGCCATTGTGTTTTTCTTCTGACTTGCTTGTTCACATTGTTTACCTTGTTTTCTTCTGTCTTGTGTAGT
 26865 GTAATAGTTTAGACTCTGAAGCCAGGCAACCTGAGTTAGAAGCCAGGCCCTCTATTTTCATGATGTAGGTCTTTGGGCAAAGTACCTAACATTC
 26957 ATGCCCTTAGTGTTTCTCTTTAATGAGCAGGGATAATAATAGTACCTGCCTCCTAAGGTTGTATAAAATTAAGTGGGCACTTAGGGTAAT
 27049 ATCTAGCAGGTAGATATTGGCTATTATCAATAGTAGCTCTTATCGTTACTATTCTTCCAGATACTGTTTCTGACTCTGGGGCAAAGTCTCTG
 27141 CTACCCCTGAACCACATTTTCTACCTCTTAGATTTTACTTGGTAATTCATCAGCCACTGTTGGGCATCCTCTGTGTTTAAATGCATCATCT
 27233 TAGACCTTAGGAGGATGGGAGGAACTTAAGAAGCCGAATTTGCTTTTTATTTATCTTGTAGCAGAGCAATAGATGTATATTAGGTAGATT
 27325 ACAAGCTTTTAGGTTATTTTGCATCTAAAGCTGTCCCTCTTTTCCAATAAATGATGTCTGTGGTAAAGAATATATCTGTTGGGTGTAGT
 27417 GACAAAATCAGAAATGCTTTGTGTCTATTTTGGCTAGTAGTTAATGTTTTCTTTTATGTGTCTGCATTCTTATTTGTTCTTTAATTTATAC
 27509 CGAGCTCATTAGCAGTTATTTCTGCTTTATTCATTTCTTATCTCTAGCATAGTCAGCTCAAGACAACAAGCATCTTTCAGAAAGCCACTAG

FIG. 12B
6 of 10

27601 GAATTGCATCTACATTAAGAACCCTCTCTGCTCTAGCGCTGAGAACATAACACAGTATTTGCTTTTGTGAAGGGCTCAAGCGGACGA
27693 TTCAGAAGTAGAATAGATAAAGTGTGGTGGTGGCTTGCAGCACCTAGTACTGATGGTTTTGTTAGGAAACACCACAGGCAGTATACAATGTA
27785 AAGCAAGTTCTTTGGGTTTCAGTTAAATAGATTCCACTTGCACGTGTTCTCACTCTTTTGGTGTGAAAAATTAGGAAAGGTGATAGGCAGGAT
27877 AGAATAAAATGAAGTGGTCCCATCTCCCATATGGAGAGCGCTGCCTCCACCACAGACACATGTTTTGCCCTGGAAGCATAAACAGAAGATT
27969 GCAGGAACGCCCCCTTCACTCCATAGCCTTCAGGCTCCCATCGATAGCATCAAGATAAACTTGGTGTGGCAACAGACTTGAGCCATCATCTT
28061 GTTTAACATTTTTTACCTGGAAGTGAAAAATGGAATCCAGAGAGGCTAAGTAGCTTGACACAGCTACTTAATTGAACTAGAACCCAGAACCCAGTT
28153 TCTTAGTATTCTGGTGCCCATTTTTATATAAACATAGACAGCTGATCATGGTAGTTTGGATCATTGCTAAAGACCTATTATATACAACAATCG
28245 TATGGCTAAGAAGATTAAAGATGCTTATTTTCTCGTTATCCATGATTAGAAATGTAATAAGAGACTTTGTTCTGTCCCAACAGAAGAGACAA
28337 GACGCCCTTTTCTGCTGTGGTGTGAGTGCCCCATCAAGTGCTGAGATGTGACTCATGTCTTTGGGGAAAGTAGCAGATGAGAGAGTACATT
28429 TATTCCGACTCCATAGACTTAACTGTGGAGACTGAGAGTAGTGGAGAGCTCAGACTGACAAGAAGAACAGAATATAGACTTAGAGGCACAG
28521 GCATGAAAAATCATAAAGATGGAGATGACTTCTATCTTGTGAATGCTGAAAGCCTCTCTCTCTTTCTGTCTCCAAATCCTTCATCTCCAG
28613 CCCTCATCTCTGCCACCATCTGTCGGTTTTCTTCCGTGGCTCTCTTCTGTCTCACCTCTTCAATGTTGGGCCCCCAGGATTTTGTCTTCAGA
28705 CTCACTTTACCCCTCTCCCTCAGGACATCTCATCCACTCCCAAGGCTGGAATCCAGCCTTCTCTCAGCCTTGCGCTTAAGTTTCATCCCT
28797 TTAGCTGTCTATTGGATGTTTCCAGTTGAAATCCACAGGCATCTCTACCCAGGCGTCTCTACACAAAGATGATAAAAAATATTATCATCTT
28889 TTTGGCAGATTGTTTTTTCTGAGTTTTCTGTCTGTTCATGGATTACCATTACAGCAGGCTGCCAAGCTAGAAATGTGGGATTTGTTAAT
28981 CGGCCCTGCTGTGAGACTGGGAGGCTGGTGTGATAACCCAAGAAAGACATTGTGGGCTCTGGGTCTTATCCTTTTTTAACCCATTGCCTCAG
29073 CCCTGCCCGAGTGATGCTTCTGAAATGTGGAATCATTATTTATCTCTTACCTAAAGGTTGCAGGATATTTTAGATTCTGAATGAAATCCCC
29165 AATCCTTTTTTTTTTTTTTAAAGTGAAGCAAGTTTATTAAGAAAGTAAAGAAATAAGAAATGGCTATGCCATTGGCAAAGCAGCCCTGTGG
29257 GCTGCTGGTTGCCCATTTTTTATGTTTTTTCTTGATGATATGCTAAACAAGGGGTGGGAAATCCCCAATCCTTGGCATTCAAATCCCAGACT
29349 CATTTCTTTTCACTTTTTTTTTTAAATCATGCCCTGCCTTTCAGTTATGATGAGTGACTTGGTCATTGCTCAGGTGTGACTTGTCCCTTTC
29441 ACCTGCTGTGCCCTCTCTCTAGAAATGCGCTTTTCTCTTTTCTGGCCAAGTGTTCTGTCTCTCCAAATGGGCCCTTCCCTTGGGAGGTGGTTT
29533 CTGACGACCACCCCTTAGTCCAAGTCAGCTCCCACTGTACTTTAAACTTTCTCTGTCTCTCTTATTACCTGTTGATATGCTCTCTCCCCAC
29625 CTGGTGTCTCTTGGGACTAGGGACTTCCCTTCATTACATTTCACATAACTTGAGGGCTGGCTCATAAGAGGTGCTTAATGAATATTTATG
29717 AATTAATTAGCATCTTGCTCTTCAAGATCAGCCATCATTTTCTCTATCTCATCATTCAAAAATATATTCTTCTCTTCCCTTCTTGCACCC
29809 AGTCACAGACTGGACTCTATTAATCCTGTCTATCATCTGGGCTCATTTCCATCCTCAGTGCTGTCTGTGCATCCTTTTCACTCAGCCAGG
29901 GATGTTCACTCGATTCTGCCCTTCATTCCAAGCCTGTCCCATATTCCATTACTTTATGAAGCCTTTCTTGACACACAGATGCTTAATTAT
29993 TCTCTTTTGCTTTCTTTGTGTTGACTTTGACTCTCCCACTGGTTGTGAGCTTCAGAAGGGCAGGGATCTACCTTCACTTCTTTTCTCTCT
30085 AGTGCTTTCTTTGTGTGCTGCACACTCCCTGGCACACACAGCGGCTCTCCAACACGAGGCAGAGCTTTCCAGCAGCCTCAACCTCAGGACT
30177 GGGCAGCTTTTAAATGTATTTGGGACCTTTTGCAAGAAAAGGATTGTGTTAAATGTAATTTTCATGTATCTTGTATCAGAGTGCAAGAGAA
30269 GCAGAAATCAAATGAAAAGTGAAGCAGAGTCAAACTTTTTATTTGGACCCAGATGCCAGGTAAGAACTATCTAAATGTTTAAATATTA
30361 AAACCAAATGTGGGAGAGAAAATCATCGATGGGCTTATTTGTTTATTTGTTTGTCTTGTGTTTATTTGGAAAAACAAGCAAATAACTATAGA
30453 AAATTTGGGGAAAAGAGGAAAAATAAAAAATGATAATCTTATCACCATAGCATTACTATTGTGAATATTTGATATTCAATAGATGTTTGAAA
30545 ATTGGGAGAGATTTATTGAAAGACATTCTCAAGTTCAAAAAGAACATCTAATTTACCTGTTAAAAATAACCATCAGAAAACAACAGGTATCAC
30637 TGCAGTTGCCCTGGGAGTCAGTGATAATTCCCGACTAGCCAGGCTCAGGCTCAAATACAAACCTTTTCCATTAACTCTAACGATAAGTACT
30729 TTTCTGTTTCTCACAAACCTCATAACCATACGTATGTGTGTTTATATGTCTATATTTTTTATTTGCTTTTAAAGAGTTTTTGTGTTATCAT
30821 GTAAAAATATACATAATATAAAATTTACCATTTTAACCATTTTTAAGTGTACGGTTCAAGTGGCATTAAATACATTCTCATTGTTGTACAACCA
30913 TTACCACCATCCATTTCAGAACTTCTTCATTTTCCACACAGGAACTTTGTATCAAATGATAACCTTCTCTTCTTCCCCCATCCCCCT
31005 AGTAACCTCTGTTCTACTCTGTGAACCTGCCTATTTTTAGGAACCTCATAAATGTGGAATCATACAGTATTTGTCTTTGTTTCTGGCTTCTT
31097 AAACCTAACATGTTTTCAAGGTCAATCCATGTTGTAGCATGTGTGAGAATTTCTTCTCTTCTGTGGCTGAATATTCCATTGTATGTATATA
31189 CTACATTTTATATATCCTTGTAATCTGTTGATGGACACTTGGTTGGATACTTGATGGACATTGGTTTTGTTGTTTCATGATCATAATTTTCA
31281 AGCTCTGTATTTTTTCAAGTTTCATCCATTGAGTAGGTATACCATCATGTCTTTTTTTTTTTTGTCTTTTTTTTTTTTTTTTTTTTGGGAGAG
31373 TCTTGCTCTGTGCGCCAGGCTGGAGTGCAATCTCGGCTACTGCAAGCTCCGCTCTCTGGGTTACACACATTCTCTGCTCAG
31465 CCTCAGCCTCCCAGTAGCTGGGACCACAGGTGCCCACTACCACACTGGCTAAATTTTTTGTATTTTTTGTAGAGACGGGGTCTCACTGGG
31557 TTAGCCAGGATGGTCTCGATCTCTGACCTGGTGAGCGCCAGCCTCGGCTCCCAAAGTGCTGGAATTACAGGCGTGAGCCACCGTGGCCG
31649 GCCCATGTCTTTGACCATGTTTATAAACTATGTGTGTAACACTATAAAACATAGAAACCGATTATATAATAGCAACACTATTGTGAGTAAA
31741 TAAGTGTATATAGCTTTTCCATATTTTATCCGTTTCTTGTGATGCATTTATGATGTTTTTTTAAATAAGAGCATAACTTATTTATATGT
31833 TTACATTTTCTTTTAAAGAAGCTTGACTTCTCATCAGCTGAGCCAGAAGTGAAGTCATTGGAAGAGAAGTTTGGAAAAAGGATCCTTGTCAA
31925 GTGCAATGATTTATCTTTCAATTTGCAATGCTGTGTTGCCGAAAAATGAAGAAGGACCCACTACAAATGTAATTTTTTCATTTTAAAAATAAAC
32017 ATTAATAAAAAAATAGGCAGAGGTTTCAGATGTACCTTTACAGTGCAGCCTGGATAAGAAATCCTAGTCCCTGGTATCAAAGAGGTGCAGTG
32109 TTTGGATCAGGATATGGAGGTTGTTAGCTGCAAGGACAGGATGTTCTGTGATGGAAGATGAGGGTGGCAGGTTTGTGCTCAGCTTTCCAGGA

36801 ATACCTTTTAAATCGATATAGATAGGTGCATGGATGGGTCAATAGGCCTATTCTGTTTGTGTTTCAGAGACAAAGAGGATTTGAATGTGTAA
36893 AACTGAGAAATACATAAGCCAGATTTTGAAAAAATCATTTGGTAGAGTCACAGAGAGGATAGACACTGTCTGGAGAAGTGCTACCTGGAAC
36985 TGGCAGGGTGCACGGTAGTGTTAGCTGCAGAGCTGGGATTCAAGGACCAACCACATGCCTCCAGCTGGAAGTCAGGGCAATCCAGTGAGGC
37077 CTGGGGTGATCTTTATCTCTTGACTCTACTTGTTAAGCATTGACTTTGTGTATATTGTTTCTTAAGCACAGCCATTGGCTGGAATGTTTT
37169 CTATGTAAATTGATTTAGTTGTCCTCATCCCCATAGATGTTTTCCATGTTTTTAGATAATGAGATTTCTGTTGGCTATAGCCAAATGGAATAA
37261 TAATTAGACTTCTCATAGAACTAGACTTAAATAATGAATTGATTTTGGTGTTTTTGAAAACCCAGTTTTAGAAATGTGCTTTGCCATTTTCAG
37353 GACATTGTTTAAGGATGCATCTGGAATCTTGACAAAAATGCCAGATTTTCTGCCATCTACAGGCAAGACAGCAATAAGCTATCCAATGATG
37445 ACATGCTCAAGTTACTTGCAGACTTTTCGGAAGTGAGTTTCAAGGCTTATTTCCACACCTGAAAAATAGAAGCTGTGTAGTGGGAGGGAGG
37537 AACAGGGGAGCAGTCACTTAGGTTGCTGATTAGACATCAGAGGGGATGGCAAATGAGCGTGAAGCATTTCCTCAAACCCCTTGAGAAGAAA
37629 GATGGGGTGAAAAATCAGAAGAATAACCAAGTTAATTTGAATTCTGTAGAGGATGTTTTGGGTGGTGCTGTGAAGGGTGGACTGGGTAAGGATG
37721 AGCCTATGGTGGGGAGGAAACAGTTGAGGAACCTTGTCAGAGGTGAGAAAGGACTCAGCAAAGCCACTGCAAGTGCAAACAGGAAGAAGGG
37813 GACAAATTCAAGTCGTGCCAAAGAGATACGATGACTGGGCTTGGCTTGGGGTGGTAATAGTCTAAGATAAATAACTTGCAAGGTTTCTAAC
37905 TTGGAAGTTTCTGGCACCAGTTGTTGCTTAGCTTGTGGCAGCATTGCTCCACTCTGCCTCTGGCCTCACATGGTCCCTCTTCTGTGTGCTC
37997 TGCTCAAATTCCTTCTTAGAACACTAGTGATAAAGCATCAGGGCCAAAGCCTAGTGACCTCATCTTAAGTATTGCATCTGCAGAGACCCCTG
38089 TTTCCAAATAGGTCACATTTATAGGTACAAAGGTTGGGACTTCACCATGCTTTTGGAGGACACAATTAACCCATAACAATGAGGCAAGA
38181 GGGAGCAAGGAATGTGTCAACATCACAGGGCCGGCAGCTTCCCAAGTCAGTCTCAGCCGAGGGTCTGTGTTCTTAACCTCTATGCTGTTTT
38273 TGCTGCTACATCTAAAGAGTTCACTCTGAACCTTTGAACTGATTTCTTTGCTAGGGAGATGGGTCTTAGAATTTTTCTGGGGAAATCT
38365 GGAATGTGAAAGAGCTGAGGGCGCTAGAAGATGTGAAGTGAAGAAGATAGCTGAGAGCCAAATGCTAACTATTCTATGCCAAAGGTATCCT
38457 TGTTTTTTTTTTTTTTTGTGCATATCAAAATAGCAATCTTATCAGTTTGTCTAGAAGTCAAGAATGATTGCTTAGCTTTCTTTAACCTTATT
38549 TTACCTTTTTCTTATCTGTCTTCAGTAGTAGGAATAGAAACGATATGAGTCATAGAAACAGGCTCAATAAGTTCTGAAAACACAGAGACGTG
38641 TTCCTAATCAGAATCCAATCACGTCCATGTCAGCAGGCGGCTTCAGCCTTCACAGCGACGTGAAATCCCTTGTCAAGAGGCTCAAAAAGGTA
38733 GAAAGGATTCTCAAGGTCCTTTTCAGTTATGTGATTATACAGTTTTTGACTGTCTTGATGTTTCCCTGTTTGGAGCTTTAATGAGAAGTGC
38825 AACCTCAGTTTTTGCTAACATGCAGCTAAGGTTGGCCTGTTTCAGCAAAGCAGTGTGCATGCCCCTGGGCTGATTGGAATGAACCTTTTACA
38917 GCTCACGTAGGGAATTGGAAGGGGGAGAGGAGGATACTGGTGAAGGATGAGGCCTGCTGGGTAGCCTTCCAGGGTTCCTGGACCATAATA
39009 GGTGCCCCAAATTCAGTCACTATCTGACAGTTTTATGACCTGGTAAGGACACAGGCTCTGGCCAGGGAGTGCCCTGGATCCCTATGAAT
39101 CTGTTATTCATGAAAGACTAAATAAAAGAATAGTACCCTATTTTTACTTTTTAAATCATAGAGGTTCTTTAGTTTACAAACATAATACATGTT
39193 CATTTTAGAAAATTTTGAGAAATACAGAAGAATAAAAGGATGAAAAAAGGTTTACTACTAGTTTAACTTCGTGGTGAAGTTTGGAGAACT
39285 TTTTTTTTTTTTTTTGAGATGGAGTCTCACTCTGTCCCTCAGGCTGGCGTACAGTAGCAGGATTTAGCTCACTGCAACCTCCGCTCCCGAG
39377 TTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTATAGGCGCCACCCTACGCTGGCTAATTTTTGTATTTTATAGTAGAGA
39469 TGGGGTTTACCATATTTGGCCAGGCTGATCTCAAACCTGCTGACCTTGTGATCTGCCCCGCTCAGCCTCCCAAGTCTGGGATTACAGGCAT
39561 GAGCCACCGTGCCAGCCTAGGGGGGAACATTTTTTTTTACGTTTTATTCCCTTACATTTTATTTTAGTTTATCTTATGTAGCTATGATCAT
39653 ACTAAATATGTAATATTTCCCTGCACAACCTCAAGTATTTCTGAAAGTGTTATATATACATTTTATAGACATCATTTTAAATGCATAAATA
39745 TTATAATAGTCCATTGAGATAGACCATAGATTATTTAACTCTTCCCCCATTTTTTGACTTTTTTTTTTTTTTCCGAGATGGAGTCTCGCTCT
39837 GTCGCCAGGCTGGAGTGCAGTGGCACCATCTCAGTCACTGCAACCTCCGCTCCAGGTTCAAGCAATTCTCCTGCCTCAGCCTCTGAGT
39929 AGCTGGGACTCCTGAGTAGCTGAGTAGCGCATGCTGCCACGCCCCGCTAATTTTTTTTTTTTTTTTTTTTTTTTGTATTTTAGTAGAGA
40021 TACTAAATATCTCACCATCTTGCCAGGCTGGTCTCAAACCTCTGACCTCAGGCAATCTGCCCGCTCAGCTTCCCAAAGTCTGGGATTAC
40113 AGGTGTGAGCCACCATGCCAGCATTTTTTGACTTTTAATGTGTTCTGATTTTTCAGAATTATACCTATAAGCCACAGTTAGAATCTTTA
40205 AAAAAATCTTCTCTATTGGTAGTGGGTAATATATTATCATACATACTATATTATCATATAGTAATTATTGTCAATTTTTGAGTTTCAAGAAA
40297 ATTTCAITCTTACTAATTTTTTCAAAAACCAAGTCACCTTTAGTTGGATAGATTCAATATTTTCTTCTGCTCAACTACCATGCAACTCTTAA
40389 TAACCATGAGGTGGGTCTGCGTGACTTAGGAAAGTGAATACACTATATTATTAAGGAAGAAAAAATATATCTGTATTACTATATTTTTTGA
40481 AAGAAAATATATATTTCTTTTGTATGTAATGAAGAAATGGATAAGCAAGTAGCTATCTAGATGGAAAGATAGGCATAAAAATAGCTATTTA
40573 GGATATATGCCAAATAATCATGGTTATCTCTGAGGATGGGTTGATGGGTGATTTTACCTTCCACTTTATAACATTCTGTCATTTTATA
40665 TGAACTTTTAAAAAATAACACTTTTATATTAGACAAAAACAATGAAGTTTTTTATATGTGATGGAGGTTGGAGCCCTGTCTCAGAAG
40757 TTACTTCTTAGGCTGGTTAGCTTGAGACTTCCCAAGTGGCGGCTCTCAGGGGAGCCCAAGTGCATGGTCTGTCTCAGTGGAGGCTG
40849 GGGAGTGGGGCTTCACATGGTCATAATTGAAAGTGATGGGAGCAGAAAGCCTGTGGCCAGGCAGAAAGGAGCCAGGGAAAACCAAGTGT
40941 GAGTTCTCTTCTGCACACCACTTCTTCATGCATGTGCTCAGCAGGAGGGCATTGGTGTGAAGGGTGTGCTCCAGGTGGCCAGTTAGAGACCC
41033 AGAAACCTGAAACAGGGATCCGATGGTGACAGCATAGAAGACACAGCAGGATAAGTGAGGCCACGCTCCTCAATAAGTATTCAAAGAACT
41125 TTGGTGCCCACTCCCGTATTCTTCACAACAGAGTTAGGGGACGTGGAGGATTCTTTTTCATTTTTTAAAAATCTTTGCATTGCTATTTTT
41217 CTTTCTCTGTATATTTTACAGGAAATAATCTCATGTGAGTGGCTGGGCACCGGCTTGATCCAAAGCTATTGTTTCTACCCCATGATTG
41309 TCTCAAAATGTTATTTAATAATGCATGAAAAAATTTCTTACGCTGTCTCAGTCTTAACAAAACAGCTGCCAAAGCTCATAAGCCACTTTC

FIG. 12B

41401 CTTTTTCCCTTGCAATAATTACCCAGGGATATGTTCCAAGATTTAGTAAGAAAGCGATTCTGTCCGATAGATGATATTGCTAACATTTTATA
 41493 AGAAGAGAGACTTGGTACTTTGTATTTGATTTGTTTCATGGTGGTATCTCATGGATAAGATGGTATCTCATCTTTTCCAACCTCTGCAGGAAA
 41585 TGCGAAGACATGAAGGCAAAGTATAAAAAATAGAACGTTTTCTTTAAAACGTAGACCTTTTAAATGGTACTACGTTGGATAGTTTAGGTAATA
 41677 ATACTACTAAAGTTTTTGCCTATGCAGCTTAATGTGTCTGTGTTTATTTGTACACTCATCTTCTTTGCATCCAGGTTTACAGTCTTACCCC
 41769 GATTTCTGCTCTGGTTTACACTGCACTCAAGCCAAGTAGGGCTGCTTGACTTTCTCTAAACCCACTGGGGACTTCCCTCTGCCATGCTTTTCTC
 41861 TCTGCCCCAAATTGTGTCCCTTCCTGCCTCATCAAGCAGCACATAAATCACAAACACATGCAGCATACACACTTCCCTTTTCTTTGTCTT
 41953 TCTCAGGGAACCTTACTCATCTTTCAAAGCCCAAGTCTGTGGCTCACTTCTGTGCTGGGAGTCTTGGAGCGGTTACTTGGCTTCTCTGCCTG
 42045 AGCCGCTCTCTTTTAAAGGTGGATAAATAACAGCCCCGCCCCCTAAAACCGTGGTGGGAATAAATGCAAAAGGCATTAAGGTGATTTT
 42137 TCCCACCATGAATACTGATCTCATCCCGTGTTCCTCTCGATAGATCTAGATACTCTGCCTTCTGGTAGAGGTTTGTACATACTCTGTGAAA
 42229 GTGATTGCCCTCATATGCCGTAAGTAGCTTACAGTGTCTACTGGACTTTTGGCTTCTTGAGGAAAGAAATTATGTCTTGTGTTGCATTCCCTCC
 42321 ATGGTCTGAGTACATACATTGCAGCATATCCTAAGCACTTGATAAATGCTTATTGAATTTTCTTCTTAGACATAAACTCAGTGGTTTTGT
 42413 TGAAACAAAAATATCTCAAATTTCTTTCAATCATATATAGTTGTTTTTTTTTAAAGTGACACCAAAGCTTTTAGGGAATATTTCTTTTCAAA
 42505 AACACAGTTAGAAGATTAAACTCACCACCAATAGCAGTCCAAACATACCTGTATTGCCAGCTAATCATTTTTAACGAGCCAATACAGGAAGTC
 42597 AGGAAGGGAAGACCGGCTGCAGAAACACTTAGATAAGGACCCCAAATCTGTTGGCATGGGAGGACTGCTAGTTGATGATACCATTCCCATTT
 42689 CCTCTGTGGGAATTGTTGAGTCAGCAGAAATGGATGGGCAGTGGGAAGGGAAAATTTTCTTAAGAGAGAGTTTGAGCCTCACTTCTACATTC
 42781 ACACAGAGACAGGAGCAGTTCCAGAGGCCAGGCATCTGCAAGTGTCTGTATTGCATGCTTACTTAATTCGTGTAATTTAAGATGAGTTT
 42873 TCATGTTCAAGGATTATTTTATAAATTTTGCATAGAATATAGGTACTCTTTAGCAAAACAAAGCAAAAAAACCAAACTATTCTCAGTCATG
 42965 AAAGAATTCAGTTTGTGTAACACGCACACAACCACCACTTTGGAAGTGCATAAAAAGGCAGTAAATCTTTATTGCCTGTGAGTGTGATG
 43057 TCTAATAAACCAGATTCAACATAAACCATAAACTTTTGAATGGGTTTGAAGTTGGGTTTTTAAAAACTTAAAGCTGGCAAAAAAAAAACA
 43149 ACTTTTAAAGCCCATGTGCTACATAATATGGAATAAATCAGAAATGTGCTTGGAACACATGGAAAGAACGTCTTTACAGAAGCAGCAA
 43241 CTAGAAGTAAATCTCTCAGCAGAGGGAGGAAATAGAATAAGAAATAACTATAGTTAGGCACAGAAGGACACAATACACTATAGGAAGATTT
 43333 CCAGTGAAGATCATTTAATTAAATATGTTGCTTAGAAACGTATTTTAAATGTGTTCCACCTCTCTCAAAATTTATATGTGGAGGATGTTG
 43425 GAGTGATCTTAAAAATGGTGATGAAGATGCCTGTTCATTATAGGTGGAAATAATTAGGAGGGGTGAAATCCATTACCCCTGCATACTTAC
 43517 TTATATTTAAAGTATAATTGTAATAAA

```

hCLASP4 -----MFPMEDISISVIGRQRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGOYSGSPQLLKNLNIVG 41
hCLASP2 -----MLLFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFKEPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      ...

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHV VNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAE EEAQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDA EHKAE NLLVKEACKFYSSQWHV VNYK 120
      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECRTEP-GIPKD-EKLDAQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
      :: .      : * .      : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSIILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNSYQDDQDDLKRRSMI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLDGGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTDTQ RERQKG-LPRQVFEQDASGDERSGPEDSNDSSRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLD SCT 239
      : :      : :      *      : :      : :      : :

hCLASP4 DVVQCPKMRRHAFELKMLDKYSHYLA AE TEQEME EW LITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKG PVTACDFDLRS LQPDKRLENLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRG SWACSI FDLKNSLPDALLPNLLDRTPNEEIDRONDDORKSN-----RHKE 234
hCLASP2 GVVQNNKVRRAFELKMQDKSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSIFDLRNLAADSLPSLLERAA PEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMN DLT YFVLA AE TESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : :      : :      : :      : :

hCLASP4 TAQDD ETSS---QGKAENIMASLERSMHP ELMKYGRETEQLNKL SRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD---EEDAVEIRPVPEC PKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD---EEEP IERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD---EQSKLEGSGGLDSYLP ELAKSAREAEIK---LKSES RVKLFYLDPD 272
hCLASP7 LLTLYPAPD---EDEAVERCSRPEPPREHFG-----QRILVKCLSLKFEIE 273
hCLASP1 TDLGLDSL DNSVTCECTPEETDSS ENNLHADFAKYLTETEDTVKTRNMERLNLFS LDPD 359
      .      :      :      : : :

hCLASP4 VQRLDFS---GIEPDIKP-FEEKCNKRFLVNCHDLTFN ILGQIGNAKGPPTNVEPFFI 333
hCLASP5 IEPLFAS---IALYDVKERKKI SENFHCDLNSDQFGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS---LALYDVKEKKK ISENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQKLDFS---SAEPEVKS-FEEKFGKRI LVKCN DLSFNLQCCVAENE EGPTTNVEPFFV 327
hCLASP7 IEPIFGI---LALYDVREKKK ISENFYFDLNSDSMKGLLRAGH THPAISTLARSAIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKA AKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
      : :      : :      : :      : :      : :      : :      * : .

```

FIG. 13
1 of 6

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNEFFQYCQKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREKD-----MSQSPTS NFIRSCKNLLNVE	887
	.. *:: .** :.. ** : ..	
hCLASP4	EIQVMIQFLPVILMQLER-----VLTNMTH-----EDDVP	824
hCLASP5	RIEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQHG	775
hCLASP3	QLEPVVRFLHLLLDKLIILLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHDQHG	840
hCLASP2	EGHVMIAFLPTILNQLER-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGA FEAMAHVSVLSVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLFK-----VLVQNE-----EDEIT	916
	. : : * : * : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHYVFRLEPVQRDVPKSGAPTALLDPRSHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLPNTYPNSSSPG-PGGLGGSVHYATMARSAPASLNLNRSRSLSN	899
hCLASP2	VNVTRV-I IHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSY YCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKSNI-----	972
	:	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MNVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLP TKKLFHEELALQWVVCSGSVRESALQAWFF FELMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAIILKSM	995
	. . . : ***	
	Cadherin Cleavage	
hCLASP4	ATYLLEENKIKLHGRQFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEPRTRFSDFRMDITTIVNVVTSEIAALLVKPKENEQA EKMNISLAF	970
hCLASP3	VHHLYFNDKLEAHRKSRFPERFMDDIAALVSTIASDIVSRFQKDTEM---VERLNTSLAF	1076
hCLASP2	AQHLIENSKVKLLRNQRF PASYHHAAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTERKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNPSLAF	999
hCLASP1	AQHLLIDTNKIQLERFPQFPESYQNELDNLMVMSDHWIWKYKDALEE---TRRATHSVAR	1052
	. : : . * * . : . : : . . . * : *	
hCLASP4	FLKRCCLTMDRGFIENLINDYISGFSPKDP-----KVLAEYKFEFLQTCNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVENLIRHYCSQLSAKLSNL---ETLISMRLEFLRLCSHEHYLN LNL	1027
hCLASP3	FLNDLLSVMDRGFVESLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLR ICSHEHYVT LNL	1136
hCLASP2	FIKRCFTFMDRGFVEKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVESLVRAHYKQVATRLQSSPNPAALLTLRMEFTRILCSHEHYVT LNL	1059
hCLASP1	FLKRCFTFMDRGCFVEMVNYYISMFSGGDL-----KTL CQYKFDFLQEV CQHEHFIP LCL	1107
	* : : : * * : * * : : : * : * : * : *	

FIG. 13
3 of 6

Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGI LLRETSI 1060
hCLASP5 FFMNADTAPTSP--CPSISSQNSSSCSSFQDQKIASMFDLTSEYRQQHFLTGL LFTELAA 1085
hCLASP3 PCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVPFQQHYLAGI VLTELAV 1196
hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFNRHFLVGI LLREVTG 1052
hCLASP7 PCCPLSPPASPSPSVSSSTTSQSSTFSSQAPDPKVTSMFELSGPFQQHFLAGI LLTELAL 1119
hCLASP1 PIRSANIPDPLTP-----SES----TQELHASDMPEYSVTNEFCRKHFLIGI LLREVG 1157

.: : : : *

hCLASP4 ALQDN---YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQLYLPFVGLLENIDRL 1116
hCLASP5 ALDAEGEGISKVORKAVSAIHSLSSHDLDPRCVKPEVKVIAALYLPLVGI ILDALP-- 1143
hCLASP3 ILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDPQIKARVAMLYLPLIGI IMETVP-- 1254
hCLASP2 ALQEFR---EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI 1108
hCLASP7 ALEPEAEGAFILHKKAISAVHSLLCGHDTPRYAEATVKARVAELYLPLLSIARDTLP-- 1177
hCLASP1 ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQAIASLYMPPLYGMLLDNMPRI 1213

* : : : * : : : *

hCLASP4 AGRDTLYSCA-----AMPN-S---ASRDEFPCGFTSPANRGSLSLTDKDTAYGS 1160
hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162
hCLASP3 -----QLY-----DFTETHNQRGRPICIAATDD-- 1276
hCLASP2 NVRDVSPFPVNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167
hCLASP7 -----RLH-----DFAEGPGQRSRLASMLDSDE 1201
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFSKDVLSIAAFSSIAIS 1273

:

hCLASP4 FQ-NHGHIKREDSRGS LIPEGATGFPDQNGTGEN-----TRQSSTRSSVSQYNRLDQYE 1213
hCLASP5 -----EEQEGAGAINQNVALAIAGNNFNLT-----SGIVLSSLPYKQYNMLNADT 1208
hCLASP3 -----YESESGSMISQTVAMAIAGTSVPQLTR-----PGSFLLTSTSGRQHTTFSAES 1324
hCLASP2 STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQQSSTLGNSVVRCDKLDQSE 1227
hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALSAES 1249
hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327

: : : :

hCLASP4 IRSLLMCYLYIVKMISEDTLTYWNKVSPQELINILILLEVCLFHFYRMGKRNIARVHDA 1273
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKKGQSSDKVSTQ 1268
hCLASP3 SRSLICLLWVLKNADETVLQKWFTDLSVLQNLRLDLLYLVCVSCFEYKKGKVFERMNSL 1384
hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSELMDDFTISEVCLHQFYMGKRYIARNQEG 1287
hCLASP7 SRTLLACVLWVLKNTPEALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKKGKAFERINSL 1309
hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQRAPSPEVSDFFSILDVCLQNFYRLGKRNIIRKIAA 1387

.: * * : : : : : : : : * * * :

hCLASP4 WLSKHFGIDR-----KSQTMPALRNRSGVMQARLQHLSSLESS----- 1311
hCLASP5 VLQKSRDVKAR-----LEEALLRGEGARGEMMRRRAPGNDRFPGLNEN--- 1311
hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430
hCLASP2 LGPIVHDRKS-----QTLPVSRNRTGMMHARLQQLGSLDNS----- 1323
hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFNGPEN----- 1350
hCLASP1 AFKFVQSTQNNGTLKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSQLPIIRGKN----- 1442

: : :

hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFITQCFKTQLL 1359
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAEELDQEALISGNLATEAHLIILDMQENITQASS-ALD 1368
hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE 1489
hCLASP2 -----LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLL 1371
hCLASP7 --VRWRKSVTHWKQTSRVDKTKDEMEHEALVEGNLATEASLVVLDLTLEIIVQTVM-LSE 1407
hCLASP1 --ALSNPKLLQMLDNTMTSNSNEIDIVHHVDTEANIATEGCLTILDVLSLFTQTHQRQLQ 1500

: : : : * * * * * * *

FIG. 13
4 of 6

hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIAKFGDLLFEEVEQCDFDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFAQALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQALVSKFPELLFEEDTELCDLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLVCKFPSAFFQGPADLCGSFCY 1560
. : : : : * * : : : * : : * : : * : *

hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCCGRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
.: : * : : : * : : : * : : : : : *

hCLASP4 SRFQESLFIINNFANSRPMKATAFPAEVKDLTKRIRTVLMATAQMKHEKDPPEMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFPPTQVEELLCNLNSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTLITYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKHEQEDPEMLIDLQ 1664
hCLASP2 TRFQQSLSIINNCANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1551
hCLASP7 EHLRRSLKTLITYAEEDMGLRDSTFAEQVQDLMFNLHMILTDTVKMKHEQEDPEMLIDLQ 1582
hCLASP1 SRFQHS LAITNNFANGDKQMKNSNFPAEVKDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1679
.: : * : : : * : : : * : : : : : *

transmembrane
hCLASP4 YSLAKSYASTPELRKTWLDMAKIHVKNGD FSEAAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLTLWLQNMMAEKHTKKKCYTEAAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEEAQLVHSAALVAEYLSMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTWLDMAKIHVKNGD LSEAAMCYVHVTALVAEYITRKG----- 1604
hCLASP7 YRIARGYQSPDLRLTLWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYIALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGD LSEAAMCYIHIAALIAEYILKRKG YWKVEKI 1739
* : : * : : * : : : * : : : : : *

hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVSSEDTLSPDEEDGV 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDVVSPEDEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD----- 1634
hCLASP7 -----RHLPGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDNSNLLTTPSGGSMFSGWPAFLSITPNIKEEGAAKEDSGMHD----- 1795
: * : * : : : * : : *

ITAM
hCLASP4 ---VHYSEEVLLELLEQCVDGLWKAERYEIISEISKLVPIYIEKRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQAALFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQAASFMSMAGMYEAVNEVYKLVIPILEANRDAKKLSTIHGKLOE 1813
hCLASP2 ---VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIYIEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLAAVHGKLOE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSEYELIADVKNPIIAVFEKQRDFKKLSDLIYYDIHR 1852
.: : * : : : : : : : : *

ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKILEVMHTKRLGLTFFRVAFYGGQFFEEEDGKEYIYKEFKLTGLSEISRLRVKIY 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEFVYKEFAITKLPEISHRLEAFY 1750
hCLASP3 AFSKIVHQSTGWERMFGTYFRVGFFG-TKFGDLDEQEFVYKEFAITKLAEISHRLEGEY 1872
hCLASP2 -----DFFEDGKEYIYKEFKLTPLSEISQRLKKIYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFFG-AHFGDLDEQEFVYKEFSITKLAEISHRLEEFY 1791
hCLASP1 SYLKVAEVVNSEKRLFGRIYRVAFYGGQFFEEEDGKEYIYKEFKLTGLSEISQRLKKIYA 1912
: : : : : * : : : : *

FIG. 13
5 of 6

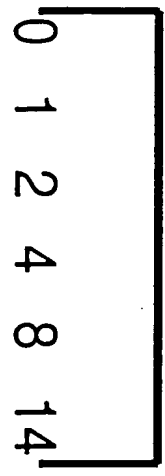
	ITAM	ITAM	
hCLASP4	ERFGTENVKIIQSDSKVNAKELDPHYAHIQVITYVKEYFDDKELTERKTEFERNHNISRFV		1799
hCLASP5	QCFGAEFVEVIKDSSTPVDKTKLDPNKAYIQITFVEEYFDEYEMKDRVTYFEKNFNLRRFM		1810
hCLASP3	ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEEYFDITYEMKDRITYFDKNYNLRRFM		1932
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIEFFDEKELQERKTEFERSHNIRRFM		1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSQKAYIQITYVEEYFDITYELKDRVTYFDRNYGLRTFL		1851
hCLASP1	DKFGADNVKIIQDSNKNVNPKDLDPHYAYIQVITYVTEFFEEKEIEDRKTD FEMHNNIRFV		1972
	: ** : *::** * : .*** :**** :* :*: * : * * : .. : * :		
		ITAM	DOCK motif
hCLASP4	FEAPYTLSGKKQGCIEEQCKRRTILTTSNSFFYVKKRIPINCEQQINLKPIDGATDEIKD		1859
hCLASP5	YTFPFTLEGRPRGELHEQYRRNTVLTTHAFFYIKTRISVIOKEEFVLTPIEVAIEDMKK		1870
hCLASP3	YCTPFTLDGRAHGEHQFQRKRTILTTSHAFFYIKTRVNVTHKEEILTPIEVAIEDMQK		1992
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILTAIHCFYVKKRIPVMYQHHTDLNPIEVAIDEMSK		1830
hCLASP7	FCTPFTPDGRAHGEHQHKKRRTLLSTDHAFFYIKTRIRVCHREETVLTPEVAIEDMQK		1911
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILTSHLFFYVKKRISQSSBELNPIEVAIDEMSR		2032
	: ** : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *		
	Coiled-coil		
hCLASP4	KTAEQLKCSSTDVDMIQQLKLQGVSVQVNAGPLAYARAFNLDSQASKYPPKKVSELK		1919
hCLASP5	KTLQLAVAINQEPDDAKMLQMVLCQSVGATVNOGPLEVAQVFLAEIPADPKLYRHHNKLK		1930
hCLASP3	KTQELAFATHQDPADPKMLQMVLCQSVGTTVNOGPLEVAQVFLSEIPSDPKLFRHHNKLK		2052
hCLASP2	KVAELRQLCSSAEVDMIKLQLKLQGVSVSVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLK		1890
hCLASP7	KTRELAFAEQDPPDAKMLQMVLCQSVGPTVNOGPLEVAQVFLAEIPEDPKLFRHHNKLK		1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLQGVSVSVKNAGPMAYARAFLEETNAKKYPDNQVKLLK		2092
	*. : * * : * * : * * : * * : * * : * * : * * : * * : * * : * * : *		
	Coiled-coil		
hCLASP4	DMFRKFIQACSALELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIHEQILQEDTMHSP		1979
hCLASP5	LCFKEFIMRCGLAVEKKNRLITADQREYQQLKKNYNKLKENLRPMIERKIPELYKPIFR		1990
hCLASP3	LCFKDFTKRCEADALRKNKSLIGPVQKEYQRELGLKSSP-----		2090
hCLASP2	EVFRQFVEACGOALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEKTS-		1949
hCLASP7	LCFKDFCKKCEADALRKNKALIGPDQKEYHRELERNYCRLREALQPIILTQRLPQLMAPTP-		2030
hCLASP1	EIFRQFADACGOALDVNERLIKEDQLEYQEELRSHYKMDLSELSTVMNEQITGRDDLKSR		2152
	* : * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *		
	PDZ ligand		
hCLASP4	WMSNTLHVFCASISGTSSDRGYGSPHYAEV--		2008
hCLASP5	VESQKRDSFHRSSFRCETQLSQGS-----		2015
hCLASP3	-----		
hCLASP2	VLPNSLHIFNAISGTPTSTMVHGMSSTSSVV		1980
hCLASP7	--PGLRNSLNRASFRKADL-----		2047
hCLASP1	GVDQTCRTRVISKATPALPTVSISSSAEV--		2180

FIG. 13
6 of 6

Human CLASP-2 expression in T cells upon activation

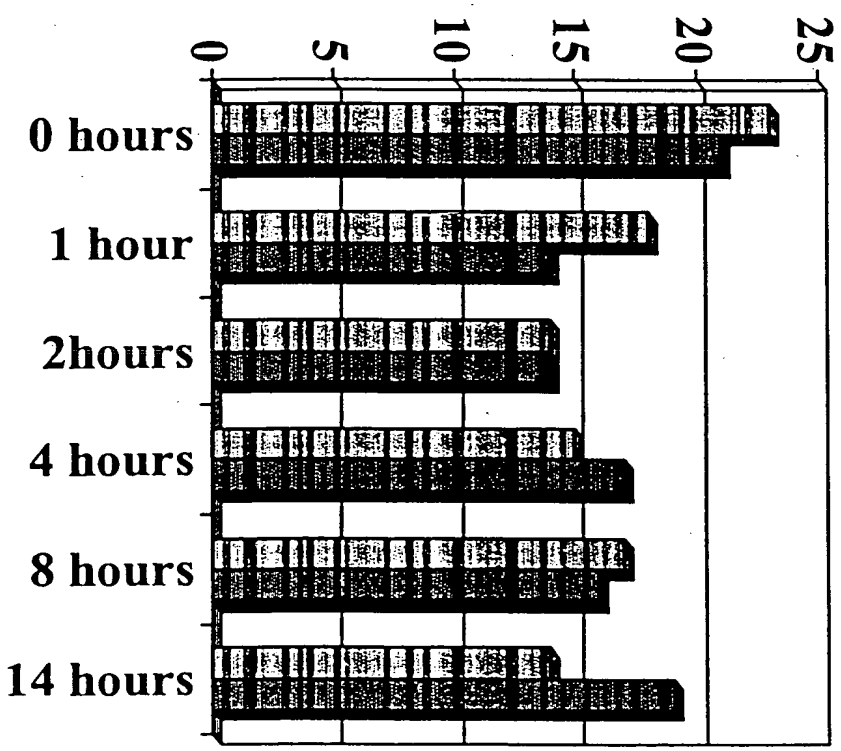
A)

hours post
activation



B)

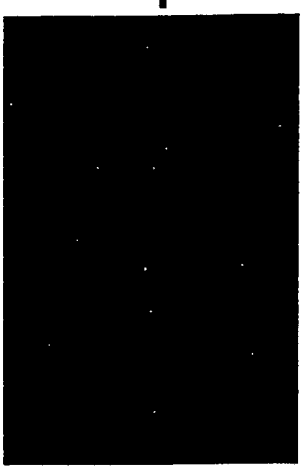
% of total
signal



CLASP-2 (A)
CLASP-2 (B)

~ 7.5 kb -

2.5 kb -



28s rRNA Ethbr. staining

TT	TTT	ACC	AAG	AAG	AAA	GAT	TTG	TTC	AGC	CTG	GTG	ACG	CTT	CAG	AAG	AGA	AGA	GTT	-52	
																		1		
TAA	CGA	CAT	TGA	TAT	TTT	GAA	ATA	TTT	TGT	GAC	TCA	AAT	TAT	AGC	AAT	ACG	ATG	AGT	TTT	9
																			met ser phe	
CGA	GGG	AAG	GTT	TTT	AAA	CGG	GAG	CCC	AGT	GAA	TTT	TGG	AAG	AAG	AGA	CGA	ACT	GTG	AGG	69
arg	gly	lys	val	phe	lys	arg	glu	pro	ser	glu	phe	trp	lys	lys	arg	arg	thr	val	arg	
AGA	GTA	ATC	CAA	GAA	GAA	TTC	CAC	AGA	TTT	AGT	TCT	CAA	GAA	AAG	CCT	AGG	CTT	CTC	GAG	129
arg	val	ile	gln	glu	glu	phe	his	arg	phe	ser	ser	gln	glu	lys	pro	arg	leu	leu	glu	
CCT	TTG	GAT	TAT	GAG	ACT	GTC	ATT	GAA	GAA	CTT	GAA	AAG	ACC	TAC	CGG	AAT	GAT	CCT	CTT	189
pro	leu	asp	tyr	glu	thr	val	ile	glu	glu	leu	glu	lys	thr	tyr	arg	asn	asp	pro	leu	
CAA	GAT	CTC	TTG	TTC	TTC	CCC	AGT	GAT	GAC	TTT	TCA	GCA	GCC	ACA	GTT	TCC	TGG	GAT	ATC	249
gln	asp	leu	leu	phe	phe	pro	ser	asp	asp	phe	ser	ala	ala	thr	val	ser	trp	asp	ile	
CGC	ACG	TTG	TAC	TCA	ACA	GTA	CCT	GAA	GAT	GCA	GAG	CAC	AAG	GCA	GAA	AAT	TTA	CTG	GTT	309
arg	thr	leu	tyr	ser	thr	val	pro	glu	asp	ala	glu	his	lys	ala	glu	asn	leu	leu	val	
AAG	GAG	GCT	TGT	AAA	TTT	TAT	AGT	TCC	CAG	TGG	CAT	GTG	GTA	AAC	TAC	AAA	TAT	GAA	CAA	369
lys	glu	ala	cys	lys	phe	tyr	ser	ser	gln	trp	his	val	val	asn	tyr	lys	tyr	glu	gln	
TAT	TCT	GGA	GAC	ATT	CGA	CAG	CTA	CCC	CGA	GCA	GAA	TAC	AAA	CCA	GAG	AAG	CTT	CCT	TCA	429
tyr	ser	gly	asp	ile	arg	gln	leu	pro	arg	ala	glu	tyr	lys	pro	glu	lys	leu	pro	ser	
CAT	TCC	TTT	GAG	ATT	GAC	CAT	GAA	GAT	GCT	GAT	AAG	GAT	GAA	GAT	ACC	ACT	TCC	CAC	TCG	489
his	ser	phe	glu	ile	asp	his	glu	asp	ala	asp	lys	asp	glu	asp	thr	thr	ser	his	ser	
TCT	TCC	AAG	GGG	GGT	GGA	GGA	GCG	GGA	GGA	ACT	GGT	GTT	TTC	AAG	TCC	GGC	TGG	CTC	TAC	549
ser	ser	lys	gly	gly	gly	gly	ala	gly	gly	thr	gly	val	phe	lys	ser	gly	trp	leu	tyr	
AAG	GGG	AAT	TTT	AAC	AGC	ACC	GTG	AAC	AAC	ACC	GTT	ACT	GTT	CGG	TCA	TTC	AAA	AAG	CGC	609
lys	gly	asn	phe	asn	ser	thr	val	asn	asn	thr	val	thr	val	arg	ser	phe	lys	lys	arg	
TAC	TTC	CAG	CTG	ACT	CAG	TTA	CCA	GAT	AAC	TCC	TAC	ATT	ATG	AAC	TTT	TAC	AAA	GAT	GAG	669
tyr	phe	gln	leu	thr	gln	leu	pro	asp	asn	ser	tyr	ile	met	asn	phe	tyr	lys	asp	glu	
AAA	ATA	TCC	AAA	GAG	CCC	AAA	GGA	TGC	ATC	TTT	TTG	GAT	TCC	TGT	ACA	GGA	GTG	GTG	CAG	729
lys	ile	ser	lys	glu	pro	lys	gly	cys	ile	phe	leu	asp	ser	cys	thr	gly	val	val	gln	
AAT	AAC	AGA	CTA	AGA	AAA	TAT	GCC	TTT	GAA	TTG	AAA	ATG	AAT	GAT	CTG	ACC	TAT	TTT	GTG	789
asn	asn	arg	leu	arg	lys	tyr	ala	phe	glu	leu	lys	met	asn	asp	leu	thr	tyr	phe	val	
CTG	GCA	GCT	GAA	ACA	GAG	TCA	GAT	ATG	GAT	GAA	TGG	ATC	CAC	ACC	CTC	AAC	CGC	ATT	CTG	849
leu	ala	ala	glu	thr	glu	ser	asp	met	asp	glu	trp	ile	his	thr	leu	asn	arg	ile	leu	
CAA	ATC	AGT	CCT	GAG	GGG	CCC	CTC	CAA	GGG	AGG	AGG	AGC	ACA	GAG	CTC	ACT	GAT	CTG	GGT	909
gln	ile	ser	pro	glu	gly	pro	leu	gln	gly	arg	arg	ser	thr	glu	leu	thr	asp	leu	gly	
CTG	GAT	TCG	CTG	GAT	AAT	TCT	GTA	ACT	TGT	GAA	TGC	ACG	CCA	GAG	GAA	ACA	GAT	TCT	TCA	969
leu	asp	ser	leu	asp	asn	ser	val	thr	cys	glu	cys	thr	pro	glu	glu	thr	asp	ser	ser	
GAG	AAC	AAC	CTA	CAC	GCA	GAC	TTT	GCA	AAG	TAC	CTC	ACA	GAA	ACA	GAA	GAT	ACT	GTA	AAA	1029
glu	asn	asn	leu	his	ala	asp	phe	ala	lys	tyr	leu	thr	glu	thr	glu	asp	thr	val	lys	
ACA	ACT	CGA	AAC	ATG	GAG	AGG	CTA	AAT	CTG	TTC	TCT	CTA	GAT	CCA	GAC	ATA	GAT	ACC	TTG	1089
thr	thr	arg	asn	met	glu	arg	leu	asn	leu	phe	ser	leu	asp	pro	asp	ile	asp	thr	leu	
AAA	CTT	CAA	AAA	AAA	GAT	CTC	TTG	GAA	CCT	GAG	TCT	GTG	ATC	AAA	CCA	TTT	GAA	GAA	AAA	1149
lys	leu	gln	lys	lys	asp	leu	leu	glu	pro	glu	ser	val	ile	lys	pro	phe	glu	glu	lys	

FIG 15/1

GCT GCC AAG AGA ATC ATG ATC ATC TGT AAA GCC CTC AAC TCA AAT CTT CAG GGA TGT GTT 1209
ala ala lys arg ile met ile ile cys lys ala leu asn ser asn leu gln gly cys val

ACG GAG AAT GAA AAT GAT CCG ATA ACG AAT ATT GAG CCT TTT TTT GTG AGT GTG GCA CTT 1269
thr glu asn glu asn asp pro ile thr asn ile glu pro phe phe val ser val ala leu

TAT GAC CTC AGA GAC AGC AGG AAG ATT TCT GCT GAT TTT CAT GTG GAT CTA AAC CAT GCT 1329
tyr asp leu arg asp ser arg lys ile ser ala asp phe his val asp leu asn his ala

GCT GTC AGA CAG ATG CTC TTG GGG GCT TCT GTG GCT TTG GAA AAT GGC AAC ATC GAC ACC 1389
ala val arg gln met leu leu gly ala ser val ala leu glu asn gly asn ile asp thr

ATC ACT CCA AGA CAA TCA GAA GAA CCT CAC ATC AAG GGA CTT CCA GAG GAA TGG CTA AAA 1449
ile thr pro arg gln ser glu glu pro his ile lys gly leu pro glu glu trp leu lys

TTT CCA AAG CAG GCT GTA TTT TCT GTA AGC AAT CCA CAT TCT GAA ATT GTT TTG GTG GCC 1509
phe pro lys gln ala val phe ser val ser asn pro his ser glu ile val leu val ala

AAA ATC GAA AAA GTC TTG ATG GGA AAC ATT GCA AGT GGT GCC GAA CCT TAT ATT AAG AAC 1569
lys ile glu lys val leu met gly asn ile ala ser gly ala glu pro tyr ile lys asn

CCA GAC TCC AAC AAG TAT GCA CAA AAG ATA CTA AAA TCC AAC AGA CAA TTC TGC AGC AAA 1629
pro asp ser asn lys tyr ala gln lys ile leu lys ser asn arg gln phe cys ser lys

TTG GGA AAA TAC CGA AGG GCT TTT GCT TGG GCA GTA AGA TCA GTA TTT AAG GAC AAC CAG 1689
leu gly lys tyr arg arg ala phe ala trp ala val arg ser val phe lys asp asn gln

GGA AAT GTG GAC AGA GAC TCA AGA TTT TCA CCA TTG TTT AGA CAA GAA AGT AGC AAG ATT 1749
gly asn val asp arg asp ser arg phe ser pro leu phe arg gln glu ser ser lys ile

TCA ACT GAG GAC CTA GTT AAA CTA GTA TCA GAT TAT AGA AGG GCC GAC AGA ATA AGC AAA 1809
ser thr glu asp leu val lys leu val ser asp tyr arg arg ala asp arg ile ser lys

ATG CAG ACC ATT CCT GGA AGC CTG GAT ATT GCT GTT GAC AAC GTT CCT TTG GAG CAT CCA 1869
met gln thr ile pro gly ser leu asp ile ala val asp asn val pro leu glu his pro

AAT TGT GTA ACA TCG TCC TTT ATC CCT GTC AAG CCT TTC AAC ATG ATG GCT CAA ACA GAA 1929
asn cys val thr ser ser phe ile pro val lys pro phe asn met met ala gln thr glu

CCC ACA GTG GAG GTG GAA GAA TTT GTT TAC GAT TCA ACA AAG TAT TGT CGG CCT TAC AGA 1989
pro thr val glu val glu glu phe val tyr asp ser thr lys tyr cys arg pro tyr arg

GTA TAT AAA AAT CAA ATT TAT ATT TAC CCC AAA CAC CTC AAG TAT GAT AGC CAG AAA TGC 2049
val tyr lys asn gln ile tyr ile tyr pro lys his leu lys tyr asp ser gln lys cys

TTC AAC AAG GCA CGG AAT ATA ACT GTG TGC ATT GAA TTC AAA AAT TCA GAT GAA GAA AGT 2109
phe asn lys ala arg asn ile thr val cys ile glu phe lys asn ser asp glu glu ser

GCC AAG CCC CTG AAG TGT ATT TAT GGA AAA CCT GAA GGG CCC CTC TTC ACC TCA GCC GCC 2169
ala lys pro leu lys cys ile tyr gly lys pro glu gly pro leu phe thr ser ala ala

TAC ACA GCA GTT CTG CAC CAC TCT CAG AAT CCG GAT TTC TCA GAT GAG GTG AAA ATT GAG 2229
tyr thr ala val leu his his ser gln asn pro asp phe ser asp glu val lys ile glu

CTA CCA ACA CAA CTC CAT GAG AAA CAC CAT ATT TTG TTT TCT TTT TAT CAC GTC ACC TGT 2289
leu pro thr gln leu his glu lys his his ile leu phe ser phe tyr his val thr cys

GAC ATC AAT GCA AAA GCT AAT GCC AAA AAG AAG GAG GCT CTG GAA ACG TCA GTT GGA TAT 2349
asp ile asn ala lys ala asn ala lys lys lys glu ala leu glu thr ser val gly tyr

GCT TGG CTT CCT CTG ATG AAA CAC GAT CAG ATA GCT TCT CAA GAG TAC AAC ATC CCA ATA 2409
ala trp leu pro leu met lys his asp gln ile ala ser gln glu tyr asn ile pro ile

FIG 15/2

GCA ACA AGT CTG CCT CCT AAT TAT TTA AGC TTT CAA GAT TCT GCA AGT GGA AAG CAT GGT 2469
ala thr ser leu pro pro asn tyr leu ser phe gln asp ser ala ser gly lys his gly
GGG AGT GAC ATT AAA TGG GTT GAT GGT GGC AAA CCA CTT TTC AAA GTG TCG ACA TTT GTT 2529
gly ser asp ile lys trp val asp gly gly lys pro leu phe lys val ser thr phe val
GTA TCA ACA GTA AAT ACT CAG GAT CCA CAT GTG AAT GCA TTT TTC CAA GAG TGC CAA AAA 2589
val ser thr val asn thr gln asp pro his val asn ala phe phe gln glu cys gln lys
AGA GAG AAA GAT ATG TCT CAG TCA CCT ACC TCA AAT TTC ATC CGC TCT TGT AAG AAC TTA 2649
arg glu lys asp met ser gln ser pro thr ser asn phe ile arg ser cys lys asn leu
TTG AAT GTG GAA AAG ATT CAT GCA ATC ATG AGT TTT CTG CCT ATA ATT TTG AAT CAG CTC 2709
leu asn val glu lys ile his ala ile met ser phe leu pro ile ile leu asn gln leu
TTC AAA GTT CTG GTA CAG AAT GAG GAA GAT GAA ATA ACT ACA ACT GTC ACC AGG GTT CTG 2769
phe lys val leu val gln asn glu glu asp glu ile thr thr thr val thr arg val leu
CCC GAC ATT GTG GCC AAG TGC CAT GAG GAG CAG CTG GAT CAT TCT GTC CAG TCA TAT ATT 2829
pro asp ile val ala lys cys his glu glu gln leu asp his ser val gln ser tyr ile
AAG TTC GTG TTC AAG ACC AGG GCA TGC AAG GAG AGG CCT GTA CAT GAG GAC CTG GCT AAA 2889
lys phe val phe lys thr arg ala cys lys glu arg pro val his glu asp leu ala lys
AAT GTG ACT GGT CTT TTG AAA TCA AAT GAC TCA CCA ACA GTA AAG CAT GTC CTA AAG CAT 2949
asn val thr gly leu leu lys ser asn asp ser pro thr val lys his val leu lys his
TCC TGG TTC TTC TTT GCA ATT ATC CTA AAA TCG ATG GCA CAG CAC TTG ATT GAC ACA AAT 3009
ser trp phe phe phe ala ile ile leu lys ser met ala gln his leu ile asp thr asn
AAA ATC CAG CTT CCC CGG CCT CAG AGA TTT CCT GAA TCT TAC CAA AAT GAA TTG GAC AAT 3069
lys ile gln leu pro arg pro gln arg phe pro glu ser tyr gln asn glu leu asp asn
CTT GTC ATG GTC CTA TCC GAC CAT GTG ATT TGG AAA TAC AAG GAT GCC CTT GAA GAA ACA 3129
leu val met val leu ser asp his val ile trp lys tyr lys asp ala leu glu glu thr
AGA AGG GCA ACC CAC AGC GTT GCC AGA TTT CTC AAG CGC TGC TTT ACA TTT ATG GAC CGG 3189
arg arg ala thr his ser val ala arg phe leu lys arg cys phe thr phe met asp arg
GGG TGT GTG TTT AAG ATG GTC AAC AAT TAC ATC AGC ATG TTC TCC TCC GGT GAC CTT AAG 3249
gly cys val phe lys met val asn asn tyr ile ser met phe ser ser gly asp leu lys
ACC TTG TGC CAG TAT AAA TTT GAT TTT CTT CAA GAA GTA TGT CAA CAT GAA CAC TTT ATC 3309
thr leu cys gln tyr lys phe asp phe leu gln glu val cys gln his glu his phe ile
CCT TTG TGT CTG CCC ATA AGA TCA GCA AAC ATT CCA GAT CCT TTG ACA CCT TCA GAA TCG 3369
pro leu cys leu pro ile arg ser ala asn ile pro asp pro leu thr pro ser glu ser
ACT CAA GAG TTA CAT GCA TCA GAT ATG CCT GAA TAT TCA GTC ACA AAT GAA TTT TGT CGG 3429
thr gln glu leu his ala ser asp met pro glu tyr ser val thr asn glu phe cys arg
AAG CAT TTC TTA ATC GGA ATT CTG CTC CGA GAA GTT GGC TTT GCC CTG CAG GAA GAC CAA 3489
lys his phe leu ile gly ile leu leu arg glu val gly phe ala leu gln glu asp gln
GAT GTC AGA CAC TTA GCT TTA GCT GTC CTA AAA AAT CTA ATG GCT AAG CAT TCA TTT GAT 3549
asp val arg his leu ala leu ala val leu lys asn leu met ala lys his ser phe asp
GAT CGA TAC AGA GAG CCA AGA AAG CAG GCC CAG ATA GCA AGT TTA TAC ATG CCC CTG TAC 3609
asp arg tyr arg glu pro arg lys gln ala gln ile ala ser leu tyr met pro leu tyr
GGC ATG CTC CTG GAC AAT ATG CCA AGG ATT TAT CTG AAG GAC CTG TAT CCT TTT ACT GTC 3669
gly met leu leu asp asn met pro arg ile tyr leu lys asp leu tyr pro phe thr val

FIG 15/3

AAT ACA TCT AAT CAG GGG TCT AGA GAT GAT CTA AGC ACC AAT GGA GGA TTT CAA AGC CAG 3729
asn thr ser asn gln gly ser arg asp asp leu ser thr asn gly gly phe gln ser gln
ACA GCT ATC AAA CAT GCA AAC TCT GTG GAT ACA TCA TTT TCT AAA GAT GTT TTA AAT TCC 3789
thr ala ile lys his ala asn ser val asp thr ser phe ser lys asp val leu asn ser
ATA GCA GCA TTT TCA TCA ATA GCT ATT TCT ACA GTA AAC CAT GCT GAC TCC AGA GCA TCT 3849
ile ala ala phe ser ser ile ala ile ser thr val asn his ala asp ser arg ala ser
TTA GCA AGT CTT GAC TCC AAT CCA AGT ACC AAT GAG AAG AGC AGT GAG AAG ACG GAC AAC 3909
leu ala ser leu asp ser asn pro ser thr asn glu lys ser ser glu lys thr asp asn
TGT GAA AAG ATC CCA AGA CCC TTG GCT TTG ATT GGC TCA ACT CTT CGA TTT GAC AGG TTA 3969
cys glu lys ile pro arg pro leu ala leu ile gly ser thr leu arg phe asp arg leu
GAT CAA GCA GAA ACC AGG AGT CTC CTG ATG TGT TTT CTT CAC ATT ATG AAA ACG ATT TCG 4029
asp gln ala glu thr arg ser leu leu met cys phe leu his ile met lys thr ile ser
TAC GAG ACT CTG ATT GCC TAC TGG CAG AGA GCT CCC AGC CCA GAG GTG TCC GAC TTC TTC 4089
tyr glu thr leu ile ala tyr trp gln arg ala pro ser pro glu val ser asp phe phe
AGC ATC TTG GAC GTT TGT CTT CAA AAT TTC AGA TAC CTA GGA AAA CGC AAC ATA ATA AGA 4149
ser ile leu asp val cys leu gln asn phe arg tyr leu gly lys arg asn ile ile arg
AAA ATT GCT GCT GCA TTT AAA TTT GTG CAG TCC ACC CAG AAC AAT GGA ACT CTC AAA GGA 4209
lys ile ala ala ala phe lys phe val gln ser thr gln asn asn gly thr leu lys gly
TCC AAT CCT TCC TGC CAG ACA TCA GGG CTC TTG GCA CAA TGG ATG CAC TCC ACT TCC AGG 4269
ser asn pro ser cys gln thr ser gly leu leu ala gln trp met his ser thr ser arg
CAT GAA GGC CAT AAG CAG CAC AGA TCA CAA ACT TTA CCT ATA ATT CGA GGC AAA AAT GCA 4329
his glu gly his lys gln his arg ser gln thr leu pro ile ile arg gly lys asn ala
CTT TCT AAC CCC AAA CTC TTA CAG ATG TTA GAC AAT ACC ATG ACC AGC AAC TCC AAT GAA 4389
leu ser asn pro lys leu leu gln met leu asp asn thr met thr ser asn ser asn glu
ATA GAC ATC GTG CAT CAT GTA GAC ACT GAG GCC AAT ATA GCT ACG GAG GGT TGC CTC ACT 4449
ile asp ile val his his val asp thr glu ala asn ile ala thr glu gly cys leu thr
ATT CTG GAC CTG GTA TCC CTC TTC ACA CAG ACT CAT CAG AGA CAA CTC CAA CAA TGT GAC 4509
ile leu asp leu val ser leu phe thr gln thr his gln arg gln leu gln gln cys asp
TGT CAA AAT TCA TTG ATG AAA AGG GGC TTT GAT ACC TAC ATG CTC TTT TTC CAA GTC AAT 4569
cys gln asn ser leu met lys arg gly phe asp thr tyr met leu phe phe gln val asn
CAG TCA GCC ACA GCG CTG AAG CAT GTG TTT GCC TCC TTG AGA CTG TTT GTA TGC AAG TTT 4629
gln ser ala thr ala leu lys his val phe ala ser leu arg leu phe val cys lys phe
CCT TCA GCG TTC TTT CAA GGG CCT GCT GAC CTC TGT GGA TCA TTC TGT TAC GAA GTC CTA 4689
pro ser ala phe phe gln gly pro ala asp leu cys gly ser phe cys tyr glu val leu
AAA TGC TGT AAC CAC AGG TCA CGG TCA ACT CAG ACA GAA GCC TCA GCC CTT CTG TAC TTG 4749
lys cys cys asn his arg ser arg ser thr gln thr glu ala ser ala leu leu tyr leu
TTC ATG AGG AAG AAT TTT GAA TTT AAC AAG CAG AAG TCA ATT GTC CGG TCC CAC TTA CAA 4809
phe met arg lys asn phe glu phe asn lys gln lys ser ile val arg ser his leu gln
CTC ATC AAA GCT GTG AGC CAG TTA ATA GCC GAT GCT GGG ATT GGA GGC TCT CGG TTT CAA 4869
leu ile lys ala val ser gln leu ile ala asp ala gly ile gly gly ser arg phe gln
CAT TCG CTT GCA ATT ACC AAT AAT TTC GCC AAT GGA GAT AAG CAA ATG AAA AAC AGC AAT 4929
his ser leu ala ile thr asn asn phe ala asn gly asp lys gln met lys asn ser asn

FIG 15/4

TTC CCA GCA GAG GTG AAG GAC CTG ACT AAG CGT ATA AGG ACT GTT TTG ATG GCC ACA GCT 4989
phe pro ala glu val lys asp leu thr lys arg ile arg thr val leu met ala thr ala

CAG ATG AAG GAG CAC GAG AAG GAC CCC GAG ATG CTG GTG GAT CTC CAG TAC AGC CTG GCA 5049
gln met lys glu his glu lys asp pro glu met leu val asp leu gln tyr ser leu ala

AAC TCC TAC GCA AGC ACT CCT GAA CTA CGC AGG ACC TGG CTG GAA AGT ATG GCC AAG ATT 5109
asn ser tyr ala ser thr pro glu leu arg arg thr trp leu glu ser met ala lys ile

CAT GCC AGA AAC GGA GAT TTA TCT GAG GCT GCC ATG TGT TAC ATC CAT ATT GCT GCT CTC 5169
his ala arg asn gly asp leu ser glu ala ala met cys tyr ile his ile ala ala leu

ATT GCA GAG TAT CTG AAA AGA AAG GGT TAC TGG AAA GTG GAA AAG ATT TGC ACA GCA TCC 5229
ile ala glu tyr leu lys arg lys gly tyr trp lys val glu lys ile cys thr ala ser

CTG CTC TCG GAG GAT ACC CAC CCC TGT GAT AGC AAC TCA TTA CTA ACA ACT CCC AGT GGA 5289
leu leu ser glu asp thr his pro cys asp ser asn ser leu leu thr thr pro ser gly

GGA AGC ATG TTC TCT ATG GGA TGG CCA GCT TTT TTG AGC ATT ACA CCC AAC ATT AAG GAA 5349
gly ser met phe ser met gly trp pro ala phe leu ser ile thr pro asn ile lys glu

GAA GGA GCC GCG AAA GAG GAT TCT GGA ATG CAC GAT ACA CCC TAC AAT GAG AAT ATC CTG 5409
glu gly ala ala lys glu asp ser gly met his asp thr pro tyr asn glu asn ile leu

GTG GAG CAG CTA TAC ATG TGT GGG GAG TTT CTC TGG AAG TCT GAG CGA TAT GAA CTC ATT 5469
val glu gln leu tyr met cys gly glu phe leu trp lys ser glu arg tyr glu leu ile

GCT GAT GTC AAC AAG CCC ATC ATT GCT GTC TTT GAG AAA CAA CGA GAC TTC AAA AAA TTG 5529
ala asp val asn lys pro ile ile ala val phe glu lys gln arg asp phe lys lys leu

TCA GAT CTC TAC TAC GAC ATT CAT CGG TCA TAT CTG AAA GTG GCA GAG GTG GTG AAT TCG 5589
ser asp leu tyr tyr asp ile his arg ser tyr leu lys val ala glu val val asn ser

GAG AAG CGG CTG TTT GGT CGC TAC TAT CGT GTG GCA TTT TAT GGG CAG GGC TTT TTT GAA 5649
glu lys arg leu phe gly arg tyr tyr arg val ala phe tyr gly gln gly phe phe glu

GAA GAA GAA GGT AAA GAG TAT ATT TAT AAA GAG CCT AAG CTG ACA GGT CTG TCC GAG ATT 5709
glu glu glu gly lys glu tyr ile tyr lys glu pro lys leu thr gly leu ser glu ile

TCC CAA AGA TTA CTC AAG CTC TAT GCA GAT AAA TTT GGA GCA GAC AAT GTG AAG ATA ATC 5769
ser gln arg leu leu lys leu tyr ala asp lys phe gly ala asp asn val lys ile ile

CAG GAT TCC AAC AAG GTA AAC CCC AAG GAT TTG GAC CCC AAA TAT GCC TAC ATC CAG GTG 5829
gln asp ser asn lys val asn pro lys asp leu asp pro lys tyr ala tyr ile gln val

ACC TAT GTG ACG CCG TTC TTT GAG GAA AAG GAA ATC GAA GAC CGG AAG ACA GAT TTC GAA 5889
thr tyr val thr pro phe phe glu glu lys glu ile glu asp arg lys thr asp phe glu

ATG CAC CAC AAC ATC AAC CGC TTT GTC TTC GAG ACA CCC TTC ACG CTG TCG GGC AAG AAG 5949
met his his asn ile asn arg phe val phe glu thr pro phe thr leu ser gly lys lys

CAC GGT GGG GTG GCG GAG CAG TGC AAG CGG CGG ACG ATC CTG ACA ACG AGT CAC CTG TTC 6009
his gly gly val ala glu gln cys lys arg arg thr ile leu thr thr ser his leu phe

CCC TAC GTG AAG AAG AGG ATC CAG GTC ATC AGC CAA TCA AGC ACA GAG CTG AAT CCT ATT 6069
pro tyr val lys lys arg ile gln val ile ser gln ser ser thr glu leu asn pro ile

GAA GTG GCA ATT GAC GAG ATG TCC AGG AAG GTC TCT GAG CTT AAT CAG CTT TGC ACA ATG 6129
glu val ala ile asp glu met ser arg lys val ser glu leu asn gln leu cys thr met

GAA GAA GTG GAC ATG ATC AGC CTA CAG CTC AAA CTG CAA GGA AGT GTC AGC GTG AAG GTT 6189
glu glu val asp met ile ser leu gln leu lys leu gln gly ser val ser val lys val

FIG 15/5

AAT GCT GGG CCA ATG GCC TAT GCA CGA GCT TTT CTT GAA GAA ACC AAT GCA AAG AAG TAC 6249
asn ala gly pro met ala tyr ala arg ala phe leu glu glu thr asn ala lys lys tyr

CCT GAC AAC CAA GTA AAG CTT TTG AAG GAG ATC TTC AGG CAA TTT GCA GAT GCA TGT GGG 6309
pro asp asn gln val lys leu leu lys glu ile phe arg gln phe ala asp ala cys gly

CAG GCC CTT GAC GTG AAT GAG CGC CTC ATC AAA GAG GAC CAG CTG GAG TAC CAG GAA GAA 6369
gln ala leu asp val asn glu arg leu ile lys glu asp gln leu glu tyr gln glu glu

CTG AGG TCC CAC TAC AAG GAC ATG CTC AGC GAA CTC TCC ACA GTC ATG AAT GAG CAG ATT 6429
leu arg ser his tyr lys asp met leu ser glu leu ser thr val met asn glu gln ile

ACG GGC AGG GAC GAC CTG TCA AAG CGC GGA GTG GAC CAA ACC TGC ACT CGA GTA ATT AGC 6489
thr gly arg asp asp leu ser lys arg gly val asp gln thr cys thr arg val ile ser

AAA GCA ACT CCG GCC CTA CCC ACG GTC TCC ATC TCA TCT AGT GCT GAA GTC TGA GAG GAA 6549
lys ala thr pro ala leu pro thr val ser ile ser ser ser ala glu val OPA

CCC TGG AGC ATC CGA TGC ACC TCT CAG AGA ACT CTC TAA ATG TTT TGC AGC TAA TCT CGG 6609
GGA AGA AAA AGA TAG ATT TAA TTT ATT TGA AGT TTT TAC AGT GTT AAT CTT GTT TAC CTT 6669
GCT AGC TTG GGA ATT TTG CCA GCC TCT GAA TTT GCA CAT TTT CTA TGA TTC CTT TGT TTC 6729
CTT GAA GTA GTA TTG ATC AAG CCA CGC TAA ACA TTT GTT CTG AAA TTC CAA TGA ACG TGC 6789
AGC TTA AAA GCA AAC TGA GTT TGC TCT TGG GTG TAA TTT GTT CAA TTC CAG GTC CTT GTA 6849
CAC GCA TTT TAG AGG TCA AAG TGA ATG TTT TTA TAA CAT TTA AGC ATA TTT CCA ATG TAA 6909
ATA GAA GAT TGT AAA ATA TAT GGT TTT TAT CAC ATT TCA AAG AAT GTT TTT AGT TGA TAC 6969
TTA TGA AAG TAC CAA AAT TAT ATG GGT AAC GTT TCA GAT CTT ATA TTA AAA TAT TTG TGT 7029
ATG TGT AAA AAC TGT TCG ATA AAT ACT AAT CTC TAA AGT TTG TGG ACT ACC TTT ATT TGT 7089
AAT ATA TGT GCT TTT AAG AGC AAT GGG ATG TGA AAT TAC AAA AAG TAT TTT GCT GTT GAT 7149
AAT ATG AAT ATG AAT AAA AAC
7170

FIG 15/6

A. Mouse CLASP-1 cDNA sequence

-169/1 -139/11
 G GAC ACT GAC ATG GAC TGA AGG AGT AGA AAG CTA CAT AGA TGT AGC ATG AGC ACT TCC
 -109/21 -79/31
 CTT CTT AGG GGA GTG GAG AGA TTT GTT CAG CCA GCT CAG TGA AGC CTC AGA AAG AAA AGG
 -49/41 -19/51
 TTT AAG GAC CTC AGT AGT TTT CAA ATA TTT TAT GAC TCC ATT TCA AGG CAT ATG ATG AGC
 met met ser
 12/61 42/71
 TTC CGA GGA AAG GAA TTC TGG AAG AGG AGG CGA ACA GTG AAG AGA GTG AAC CCA GAA GGA
 phe arg gly lys glu phe trp lys arg arg arg thr val lys arg val asn pro glu gly
 72/81 102/91
 ATC CAC AAG GCT GGT GCT CAG GAA AAG CCC AGA CTC TTG GAT CCT TTG GAT TAT GAA ACC
 ile his lys ala gly ala gln glu lys pro arg leu leu asp pro leu asp tyr glu thr
 132/101 162/111
 GTC ATT GAA GAA CTT GAA AAG ACC TAT CGG GAT GAT CCT CTT CAG GAC CTT CTG TTC TTC
 val ile glu glu leu glu lys thr tyr arg asp asp pro leu gln asp leu leu phe phe
 192/121 222/131
 CCC AGT GAT GAC TTC TCA ACA GCC ACG GTT TCT TGG GAT ATC CGA ACA CTC TAT TCG ACG
 pro ser asp asp phe ser thr ala thr val ser trp asp ile arg thr leu tyr ser thr
 252/141 282/151
 GTA CCA GAA GAG GCA GAG CAC AGG GCA GAA AGT CTG CTG GTG AAA GAG GCT TGT AAA TTC
 val pro glu glu ala glu his arg ala glu ser leu leu val lys glu ala cys lys phe
 312/161 342/171
 TAC AGT TCC CAG TGG TAC GTG GTA AAC TAC AAA TAT GAA CAA TAT TCT GGA GAC ATT CGA
 tyr ser ser gln trp tyr val val asn tyr lys tyr glu gln tyr ser gly asp ile arg
 372/181 402/191
 CAG TTG CCC CGA GCA GAA CAC AAG CCA GAG AAA CTT CCT TCA CAT TCC TTT GAG GTT GAC
 gln leu pro arg ala glu his lys pro glu lys leu pro ser his ser phe glu val asp
 432/201 462/211
 CAT GAA GAT GCT GAT AAG GAT GAA GAT ACC ACA TCC CAC TCA TCA TCC AAG GGC GGT GGG
 his glu asp ala asp lys asp glu asp thr thr ser his ser ser ser lys gly gly gly
 492/221 522/231
 GGA GCT GGA GGT ACT GGT GTG TTC AAG TCT GGC TGG CTT TAC AAG GGC AAT TTT AAC AGC
 gly ala gly gly thr gly val phe lys ser gly trp leu tyr lys gly asn phe asn ser
 552/241 582/251
 ACT GTG AAC AAT ACT GTC ACT GTT CGG TCA TTC AAA AAG CGC TAC TTC CAG CTG ACT CAG
 thr val asn asn thr val thr val arg ser phe lys lys arg tyr phe gln leu thr gln
 612/261 642/271
 TTG CCT GAT AAC TCC TAC ATT ATG AAC TTT TAC AAA GAT GAA AAG ATA TCC AAA GAG CCC
 leu pro asp asn ser tyr ile met asn phe tyr lys asp glu lys ile ser lys glu pro
 672/281 702/291
 AAG GGC TGC ATC TTT TTG GAT TCC TGC ACA GGT GTA GTA CAG AAT AAC AGG CTG AGG AAA
 lys gly cys ile phe leu asp ser cys thr gly val val gln asn asn arg leu arg lys
 732/301 762/311
 TAT GCC TTC GAG TTG AAG ATG AAC GAC CTG ACC TAT TTT GTG CTG GCT GCT GAA ACA GAG
 tyr ala phe glu leu lys met asn asp leu thr tyr phe val leu ala ala glu thr glu

792/321
 TCA GAT ATG GAC GAA TGG ATC CAC ACA CTT AAC CGT ATC CTG CAG ATC AGT CCC GAG GGC
 ser asp met asp glu trp ile his thr leu asn arg ile leu gln ile ser pro glu gly
 852/341
 CCA CTC CAG GGA AGG AAA AGT GCA GAG CTT GCT GAG CTG GGG CTA GAT CCA CTG GAT AAC
 pro leu gln gly arg lys ser ala glu leu ala glu leu gly leu asp pro leu asp asn
 912/361
 TGC GTG ACT TGT GAA TGT ACA CTG GAG GAA ACG GAT TCT TCA GAG AAC AGC CTA CAT CCT
 cys val thr cys glu cys thr leu glu glu thr asp ser ser glu asn ser leu his pro
 972/381
 GAC TTT GCA AAA TAC CTC ACA GAA ACC GAA GAC ACT GTC AAA ACA ACA CGA AAC ATG GGC
 asp phe ala lys tyr leu thr glu thr glu asp thr val lys thr thr arg asn met gly
 1032/401
 AGA CTC AAT CTG TTC TCC CTG GAC CCA GAC ATA GAC ACC CTG AAG CTT CAA AAA AGG GAC
 arg leu asn leu phe ser leu asp pro asp ile asp thr leu lys leu gln lys arg asp
 1092/421
 ATT TTT GAA AAT GAG TTG ATG ATC AAA CCC TTT GAA GAG AAA GCT GCC AAA AGA ATC ATG
 ile phe glu asn glu leu met ile lys pro phe glu glu lys ala ala lys arg ile met
 1152/441
 ATC ATC TGT AGA GCT CTC AAC TTC AAT CTT CAG GGA TGT GTT ACA GAG AAT GAA TAT GAC
 ile ile cys arg ala leu asn phe asn leu gln gly cys val thr glu asn glu tyr asp
 1212/461
 CCT GTA ACC AAT ATT GAG CCC TTT TTT GTG AGC GTG GCA CTT TAC GAC CTC AGA GAT AAC
 pro val thr asn ile glu pro phe phe val ser val ala leu tyr asp leu arg asp asn
 1272/481
 AGG AAG ATC TCT GCG GAC TTC CAT GTG GAC CTA AAT CAC CCT GCT GTC CGG CAG ATG CTC
 arg lys ile ser ala asp phe his val asp leu asn his pro ala val arg gln met leu
 1332/501
 TCG GGG ACC CCA CCG GCC TTG GAA AAC GGC AAT ATT GAC ACC GGT ACA CCA AGA CAA TCG
 ser gly thr pro pro ala leu glu asn gly asn ile asp thr gly thr pro arg gln ser
 1392/521
 GAA GAA CCT CAC ATA AAG GGC CTT CCA GAG GAA TGG TTA AAA TTC CCA AAG CAG GCT GTC
 glu glu pro his ile lys gly leu pro glu glu trp leu lys phe pro lys gln ala val
 1452/541
 TTC TCT GTG AGT GAT CCA CAC TCT GAA ATT GTT TTG GTG GCC AAA GTC GAA AAA GTC TTA
 phe ser val ser asp pro his ser glu ile val leu val ala lys val glu lys val leu
 1512/561
 ATG GGA AAC ATC GGG AGT GGT GCT GAA CCT TAT ATC AAG AAT CCA GAC TCC AAC AAG TTT
 met gly asn ile gly ser gly ala glu pro tyr ile lys asn pro asp ser asn lys phe
 1572/581
 GCA CAA AAG ATT CTA AAA TCC AAT AGG CAG TTC TGC AGC AAA TTG GGG AAA TAT CGG ATG
 ala gln lys ile leu lys ser asn arg gln phe cys ser lys leu gly lys tyr arg met
 1632/601
 CCG TTT GCT TGG GCA GTG AGA TCT GTA TTT AAG GAC AAC CAG GGG AAC GTG GAC AGG GAC
 pro phe ala trp ala val arg ser val phe lys asp asn gln gly asn val asp arg asp
 1692/621
 TCA CGG TTT TCA CCA CTG TAT AGA CAA GAA AGC AGC AAG ATG TCG TCT GAG GAC CTC CTA
 ser arg phe ser pro leu tyr arg gln glu ser ser lys met ser ser glu asp leu leu
 1752/641
 AAA CTG GTG TCA GAC TAC AGA AGA GCT GAC CGG ATA AGC AAA ATG CAG AGC ATC CCT GGA
 lys leu val ser asp tyr arg arg ala asp arg ile ser lys met gln ser ile pro gly
 1812/661
 AGC CTG GAT ATT GCT GTG GAC AAC ATT CCC TTG GAG CAC CCA AAC TGT GTA ACA TCG TCC
 ser leu asp ile ala val asp asn ile pro leu glu his pro asn cys val thr ser ser

16
Figure 1 (2 of 35)

1872/681	1902/691
TTT ATC CCT GTC AAG CCC TTC AAC GTG ACG	GCT CAG TCA GAA CCT ACA GTG GAG GTG GAA
phe ile pro val lys pro phe asn val thr	ala gln ser glu pro thr val glu val glu
1932/701	1962/711
GAA TTT ATT TAT GAC TCA ACA AAG TAT TGC	CGT CCA TAC CGA GTA TAC AAA AAT CAA ATT
glu phe ile tyr asp ser thr lys tyr cys	arg pro tyr arg val tyr lys asn gln ile
1992/721	2022/731
TAT GTA TAC CCC AAA CAC CTC AAA TAC GAT	AGC CAG AAA TGC TTC AAC AAG GCA CGG AAT
tyr val tyr pro lys his leu lys tyr asp	ser gln lys cys phe asn lys ala arg asn
2052/741	2082/751
ATA ACT GTG TGC ATT GAA TTC AAA AAT TCA	GAT GAC GAT GGA GCC AAG CCC ATG AAG TGT
ile thr val cys ile glu phe lys asn ser	asp asp asp gly ala lys pro met lys cys
2112/761	2142/771
ATT TAT GGG AAA CCT GGA GGG CCC CTC TTC	ACT TCC TCT GCC TAC ACG GCT GTG CTA CAC
ile tyr gly lys pro gly gly pro leu phe	thr ser ser ala tyr thr ala val leu his
2172/781	2202/791
CAT TCT CAA AAT CCA GAT TTC TCT GAT GAG	GTG AAA ATT GAA CTA CCA ACA CAA CTC CAT
his ser gln asn pro asp phe ser asp glu	val lys ile glu leu pro thr gln leu his
2232/801	2262/811
GGA AAA CAT CAC CTT TTG TTC TCC TTT TAC	CAC ATC ACA TGT GAC ATC AAT GCC AAA GCC
gly lys his his leu leu phe ser phe tyr	his ile thr cys asp ile asn ala lys ala
2292/821	2322/831
AAT GCC AAA AAG AAA GAG GCT TTG GAG ACA	TCA GTG GGC TAT GCA TGG CTT CCT CTG ATG
asn ala lys lys lys glu ala leu glu thr	ser val gly tyr ala trp leu pro leu met
2352/841	2382/851
AAA CAT GAT CAA ATA GCT TCT CAG GAG TAC	AAC ATC CCA ATA GCA ACG ACC CTG CCT CCT
lys his asp gln ile ala ser gln glu tyr	asn ile pro ile ala thr thr leu pro pro
2412/861	2442/871
AAT TAT TTA AGC ATT CAA GAT CCT ACA AGT	GCA AAG CAT GGT GGA AGT GAC ATT AAA TGG
asn tyr leu ser ile gln asp pro thr ser	ala lys his gly gly ser asp ile lys trp
2472/881	2502/891
GTC GAT GGT GGC AAA CCG CTT TTC AAA GTG	TCC ACA TTT GTT GTA TCA ACA GTG AAC ACT
val asp gly gly lys pro leu phe lys val	ser thr phe val val ser thr val asn thr
2532/901	2562/911
CAG GAC CCA CAT GTA AAT GCA TTT TTC CGT	CAG TGC CAA AAA AGA GAA AAA GAC ATG TCT
gln asp pro his val asn ala phe phe arg	gln cys gln lys arg glu lys asp met ser
2592/921	2622/931
CAG TCA CCT ACC TCC AGC TTT GTC CGT GCC	TGT AAG AAC TTA CTA AAT GTG GAC AAG ATC
gln ser pro thr ser ser phe val arg ala	cys lys asn leu leu asn val asp lys ile
2652/941	2682/951
CAC TCC ATC ATG AGT TTC CTG CCT ATC ATC	TTG AAC CAG CTC TTC AAA ATT CTA GTG CAG
his ser ile met ser phe leu pro ile ile	leu asn gln leu phe lys ile leu val gln
2712/961	2742/971
AAC GAG GAA GAT GAA ATT ACT GCG ACC GTC	ACC AGG GTT CTG GCT GAC ATT GTG GCC AAG
asn glu glu asp glu ile thr ala thr val	thr arg val leu ala asp ile val ala lys
2772/981	2802/991
TGT CAT GAG GAG CAA CTA GAC CAT TCT GTC	CAG TCA TAC ATT AAG TTT GTA TTC AAG ACC
cys his glu glu gln leu asp his ser val	gln ser tyr ile lys phe val phe lys thr
2832/1001	2862/1011
AAA TCC TAC AAA GAG AGA ACA ATA CAT GAG	GAA CTG GCT AAA AAT TTG AGT GAT CTT TTG
lys ser tyr lys glu arg thr ile his glu	glu leu ala lys asn leu ser asp leu leu
2892/1021	2922/1031
AAG TCC AAT GAC TCA ACG ATA GTC AAG CAT	GTT CTA GAG CAT TCT TGG TTC TTC TTT GCC
lys ser asn asp ser thr ile val lys his	val leu glu his ser trp phe phe phe ala
2952/1041	2982/1051
ATT ATT CTA AAA TCA ATG GCA CAG CAC TTG	ATT GAC ACA AAC AAA ATT CAG CTT CCC AGA
ile ile leu lys ser met ala gln his leu	ile asp thr asn lys ile gln leu pro arg

3012/1061	3042/1071
GCT CAA AGA TTC CCT GAG TCT TAC CAA AGC	GAA CTA GAC AAC TTG GTG ATG GGC CTG TGT
ala gln arg phe pro glu ser tyr gln ser	glu leu asp asn leu val met gly leu cys
3072/1081	3102/1091
GAC CAC GTG ATT TGG AAA TGC AAG GAA GCC	CCT GAG GAA ACC AAA AGA GCA AAC CAC AGC
asp his val ile trp lys cys lys glu ala	pro glu glu thr lys arg ala asn his ser
3132/1101	3162/1111
GTT GCC AGA TTC CTT AAG CGC TGC TTT ACA	TTT ATG GAC CGG GGA TTC GTG TTT AAG ATG
val ala arg phe leu lys arg cys phe thr	phe met asp arg gly phe val phe lys met
3192/1121	3222/1131
GTG AAC AAT TAC ATC AGC ATG TTC TCT TCT	GGT GAG TTT AAG ACT TTA TGC CAG TAT AAG
val asn asn tyr ile ser met phe ser ser	gly glu phe lys thr leu cys gln tyr lys
3252/1141	3282/1151
TTT GAT TTC CTT CAG GAA GTT TGT CAA CAT	GAG CAC TTT ATC CCT TTG TGT CTC CCC ATA
phe asp phe leu gln glu val cys gln his	glu his phe ile pro leu cys leu pro ile
3312/1161	3342/1171
AGA TCT GCA AAC ATT CCA GAT CCC TTG ACA	CCT TCA GAA TCA ATC CGA GAG TTA CAT GCC
arg ser ala asn ile pro asp pro leu thr	pro ser glu ser ile arg glu leu his ala
3372/1181	3402/1191
TCA GAT ATG CCT GAG TAC TCA GTC ACA AAT	GAA TTT TGC CGC AAA CAC TTC TTA ATT GGA
ser asp met pro glu tyr ser val thr asn	glu phe cys arg lys his phe leu ile gly
3432/1201	3462/1211
ATT CTT CTC CGA GAA GTT GGC TTT GCC CTG	CAG GAG GAC CAA GAC ATC AGG CAC TTA GCT
ile leu leu arg glu val gly phe ala leu	gln glu asp gln asp ile arg his leu ala
3492/1221	3522/1231
TTA GCT GTC CTA AAA AAT CTA ATG GCT AAG	CAC TCT TTC GAT GAT CGA TAC AGG GAA CCT
leu ala val leu lys asn leu met ala lys	his ser phe asp asp arg tyr arg glu pro
3552/1241	3582/1251
AGG AAG CAG GCA CAG ATA GCG AGT CTG TAC	ATG CCG CTC TAT GGT ATG CTC CTG GAC AAT
arg lys gln ala gln ile ala ser leu tyr	met pro leu tyr gly met leu leu asp asn
3612/1261	3642/1271
ATG CCA AGA ATC TAC CTG AAG GAC CTG TAT	CCT TTC ACC GTG AAC ACA TCC AAT CAG GGA
met pro arg ile tyr leu lys asp leu tyr	pro phe thr val asn thr ser asn gln gly
3672/1281	3702/1291
TCT AGA GAT GAC CTC AGC ACT AAT GGA GGA	TTT CAG ACT CAG ACG TCC ATG AAA CAT GCA
ser arg asp asp leu ser thr asn gly gly	phe gln thr gln thr ser met lys his ala
3732/1301	3762/1311
ACT TCT GTG GAT ACA TCA TTT TCC AAA GAT	GTT TTA AAT TCC ATA GCA GCA TTT TCA TCA
thr ser val asp thr ser phe ser lys asp	val leu asn ser ile ala ala phe ser ser
3792/1321	3822/1331
ATA GCT ATT TCT ACA GTG AAC CAT GCA GAT	TCC AGA GCG TCC TTA GCG AGC CTC GAC TCC
ile ala ile ser thr val asn his ala asp	ser arg ala ser leu ala ser leu asp ser
3852/1341	3882/1351
AAC CCA AGT ACC ACA GAG AAG AGC AGT GAG	AAG ACA GAC AAC TGT GAA AAG ATC CCA AGG
asn pro ser thr thr glu lys ser ser glu	lys thr asp asn cys glu lys ile pro arg
3912/1361	3942/1371
CCC TTG TCT TTG ATT GGG TCA ACG CTT CGG	TTT GAC AAA TTA GAT CAA GCA GAA ACC AGG
pro leu ser leu ile gly ser thr leu arg	phe asp lys leu asp gln ala glu thr arg
3972/1381	4002/1391
AGT CTT CTT ATG TGT TTT CTT CAC ATT ATG	AAG ACC ATT TCA GAT GAG ACT CTG ATT GCC
ser leu leu met cys phe leu his ile met	lys thr ile ser asp glu thr leu ile ala
4032/1401	4062/1411
TAC TGG CAG AGA GCA CCC AGT CCA GAG GTG	TCA GAC TTC TTC AGC ATC TTG GAC GTT TGT
tyr trp gln arg ala pro ser pro glu val	ser asp phe phe ser ile leu asp val cys
4092/1421	4122/1431
CTT CAG AAT TTT AGA TAC CTA GGG AAA CGC	AAT ATA ATA AGG AAA ATC GCT GCA GCG TTT
leu gln asn phe arg tyr leu gly lys arg	asn ile ile arg lys ile ala ala ala phe

4152/1441
 AAG TTT GTG CAG TCA ACC CAG AAC AAT GGG
 lys phe val gln ser thr gln asn asn gly
 4212/1461
 ACA TCA GGT CTC TTG TCA CAA TGG ATG CAC
 thr ser gly leu leu ser gln trp met his
 4272/1481
 CAC AGG TCT CAG ACT TTA CCT ATA ATC CGA
 his arg ser gln thr leu pro ile ile arg
 4332/1501
 TTA CAG ATG TTG GAC AAC AGC ATG AAC AGC
 leu gln met leu asp asn ser met asn ser
 4392/1521
 GTT GAC ACA GAG GCC AAC ATA GCC ACC GAG
 val asp thr glu ala asn ile ala thr glu
 4452/1541
 CTC TTT ACC CAG GTC CAC CAG AGA CAG CTC
 leu phe thr gln val his gln arg gln leu
 4512/1561
 AAA AGG GTC TTC GAT ACT TAC ATG CTG TTT
 lys arg val phe asp thr tyr met leu phe
 4572/1581
 AAA CAC GTG TTT GCT TCT TTA AGA CTG TTT
 lys his val phe ala ser leu arg leu phe
 4632/1601
 GGG CCT GCT GAC CTC TGT GGC TCA TTC TGC
 gly pro ala asp leu cys gly ser phe cys
 4692/1621
 TCA AGG TTG ACT CAG ATG GAA GCT TCA GCA
 ser arg leu thr gln met glu ala ser ala
 4752/1641
 GAG TTT AAC AAG CAG AAG TCA ATT GTC CGG
 glu phe asn lys gln lys ser ile val arg
 4812/1661
 CAG TTA ATA GCT GAT GCG GGG ATC GGA GGG
 gln leu ile ala asp ala gly ile gly gly
 4872/1681
 AAC AAC TTT GCC AAT GGA GAT AAA CAG ATG
 asn asn phe ala asn gly asp lys gln met
 4932/1701
 GAT CTG ACT AAA CGC ATA AGG ACT GTT TTG
 asp leu thr lys arg ile arg thr val leu
 4992/1721
 AAG GAC CCA GAG ATG CTG GTG GAC CTT CAA
 lys asp pro glu met leu val asp leu gln
 5052/1741
 CCG GAG TTA CGG AGG ACC TGG CTG GAA AGC
 pro glu leu arg arg thr trp leu glu ser
 5112/1761
 CTG TCT GAG GCT GCG ATG TGT TAC ATC CAT
 leu ser glu ala ala met cys tyr ile his
 5172/1781
 CGC AAG GGT TAC TGG AAA ATG GAA AAG ATT
 arg lys gly tyr trp lys met glu lys ile
 5232/1801
 CAA CCC TGT GAT AGC AAC TTA TTA CTA ACA
 gln pro cys asp ser asn leu leu leu thr
 4182/1451
 ACT CTG AAG GGA TCC AAT CCT TCC TGC CAG
 thr leu lys gly ser asn pro ser cys gln
 4242/1471
 ACA ACT TCT GGC CAC GAG GGA CAT AAG CAG
 thr thr ser gly his glu gly his lys gln
 4302/1491
 GGC AAA AAT GCA CTT TCC AAC CCC AAA CTT
 gly lys asn ala leu ser asn pro lys leu
 4362/1511
 AAT TCC AAT GAA ATA GAC ATT GTC CAC CAT
 asn ser asn glu ile asp ile val his his
 4422/1531
 GTC TGC CTC ACT ATT CTG GAC CTG CTG TCT
 val cys leu thr ile leu asp leu leu ser
 4482/1551
 CAA CAA TCC GAC TGT CAA AAT TCA CTC ATG
 gln gln ser asp cys gln asn ser leu met
 4542/1571
 TTC CAA GTC AAC CAG TCA GCC TCA GCC CTG
 phe gln val asn gln ser ala ser ala leu
 4602/1591
 GTG TGC AAG TTT CCG TCA GCG TTT TTC CAA
 val cys lys phe pro ser ala phe phe gln
 4662/1611
 TAT GAA GTC CTC AAA TGC TGT AAC CAC AGG
 tyr glu val leu lys cys cys asn his arg
 4722/1631
 CTT CTA TAC TTC TTC ATG AGG AAG AAC TTT
 leu leu tyr phe phe met arg lys asn phe
 4782/1651
 TCT CAC TTA CAA CTC ATC AAA GCA GTG AGC
 ser his leu gln leu ile lys ala val ser
 4842/1671
 TCT CGC TTT CAA CAC TCC CTT GCA ATC ACG
 ser arg phe gln his ser leu ala ile thr
 4902/1691
 AAA AAC AGC AAT TTC CCA GCA GAG GTG AAA
 lys asn ser asn phe pro ala glu val lys
 4962/1711
 ATG GCC ACA GCC CAG ATG AAG GAG CAT GAG
 met ala thr ala gln met lys glu his glu
 5022/1731
 TAC AGC CTA GCA AAC TCC TAT GCA AGT ACC
 tyr ser leu ala asn ser tyr ala ser thr
 5082/1751
 ATG GCC AAG ATT CAT GCA AGA AAT GGA GAC
 met ala lys ile his ala arg asn gly asp
 5142/1771
 ATA GCT GCA CTT ATT GCA GAA TAC CTG AAG
 ile ala ala leu ile ala glu tyr leu lys
 5202/1791
 TGC ACA CCA CCC CTG CTT CCA GAA GAC ACC
 cys thr pro pro leu leu pro glu asp thr
 5262/1811
 ACT CCA GGC GGA GGA AGC ATG TTC TCT ATG
 thr pro gly gly gly ser met phe ser met

5292/1821
 GGA TGG CCA GCC TTT CTG AGC ATC ACC CCA AAC ATT AAA GAA GAA GGA GCA ATG AAA GAG
 gly trp pro ala phe leu ser ile thr pro asn ile lys glu glu gly ala met lys glu
 5352/1841
 GAT TCT GGA ATG CAA GAC ACC CCG TAC AAT GAG AAC ATC CTG GTG GAA CAG CTG TAT ATG
 asp ser gly met gln asp thr pro tyr asn glu asn ile leu val glu gln leu tyr met
 5412/1861
 TGT GTG GAG TTC CTT TGG AAG TCT GAA CGA TAC GAA CTC ATC GCT GAT GTC AAT AAG CCC
 cys val glu phe leu trp lys ser glu arg tyr glu leu ile ala asp val asn lys pro
 5472/1881
 ATC ATC GCT GTC TTT GAA AAG CAA CGA GAC TTC AAA AAA TTA TCA GAT CTC TAT TAT GAC
 ile ile ala val phe glu lys gln arg asp phe lys lys leu ser asp leu tyr tyr asp
 5532/1901
 ATC CAC CGG TCC TAT CTG AAA GTG GCA GAG GTG GTG AAT TCG GAG AAG CGA TTG TTT GGT
 ile his arg ser tyr leu lys val ala glu val val asn ser glu lys arg leu phe gly
 5592/1921
 CGT TAC TAT AGA GTG GCG TTT TAT GGG CAG GGA TTC TTT GAG GAG GAG GAA GGT AAA GAG
 arg tyr tyr arg val ala phe tyr gly gln gly phe phe glu glu glu glu gly lys glu
 5652/1941
 TAT ATC TAC AAA GAG CCT AAG CTG ACA GGG CTC TCG GAG ATC TCC CAA AGG CTT CTC AAG
 tyr ile tyr lys glu pro lys leu thr gly leu ser glu ile ser gln arg leu leu lys
 5712/1961
 CTC TAT GCA GAC AAA TTT GGA GCA GAC AAT GTG AAG ATA ATT CAA GAC TCC AAC AAG GTA
 leu tyr ala asp lys phe gly ala asp asn val lys ile ile gln asp ser asn lys val
 5772/1981
 AAC CCC AAG GAT CTG GAC CCC AAA TAT GCC TAT ATT CAG GTG ACC TAT GTC ACA CCA TTC
 asn pro lys asp leu asp pro lys tyr ala tyr ile gln val thr tyr val thr pro phe
 5832/2001
 TTT GAA GAA AAG GAA ATC GAG GAC CGA AAG ACA GAC TTT GAA ATG CAT CAC AAC ATC AAT
 phe glu glu lys glu ile glu asp arg lys thr asp phe glu met his his asn ile asn
 5892/2021
 CGC TTT GTC TTT GAG ACA CCC TTC ACT CTG TCA GGC AAG AAG CAC GGA GGA GTG GCT GAG
 arg phe val phe glu thr pro phe thr leu ser gly lys lys his gly gly val ala glu
 5952/2041
 CAG TGC AAG CGG AGG ACA GTC CTG ACC ACA AGC CAC TTG TTC CCC TAC GTA AAG AAG AGG
 gln cys lys arg arg thr val leu thr thr ser his leu phe pro tyr val lys lys arg
 6012/2061
 ATC CAG GTC ATC AGC CAA TCA AGC ACA GAG CTG AAT CCT ATC GAG GTG GCA ATT GAT GAG
 ile gln val ile ser gln ser ser thr glu leu asn pro ile glu val ala ile asp glu
 6072/2081
 ATG TCC AGG AAG GTC TCT GAG CTT AAT CAG CTG TGC ACC ACA GAG GAG GTG GAT ATG ATC
 met ser arg lys val ser glu leu asn gln leu cys thr thr glu glu val asp met ile
 6132/2101
 CGC CTA CAG CTC AAA CTC CAG GGC AGT GTC AGC GTG AAG GTC AAT GCT GGG CCA ATG GCT
 arg leu gln leu lys leu gln gly ser val ser val lys val asn ala gly pro met ala
 6192/2121
 TAT GCT CGA GCC TTT CTT GAA GAA ACT AAT GCA AAG AAG TAT CCT GAC AAC CAA GTT AAG
 tyr ala arg ala phe leu glu glu thr asn ala lys lys tyr pro asp asn gln val lys
 6252/2141
 CTA CTA AAG GAA ATA TTC AGG CAA TTT GCA GAT GCG TGT GGG CAG GCT CTT GAT GTG AAT
 leu leu lys glu ile phe arg gln phe ala asp ala cys gly gln ala leu asp val asn
 6312/2161
 GAG CGT CTC ATC AAG GAA GAC CAG CTG GAG TAC CAG GAA GAA CTG AGG TCC CAT TAT AAG
 glu arg leu ile lys glu asp gln leu glu tyr gln glu glu leu arg ser his tyr lys
 6372/2181
 GAC ATG CTC AGT GAA CTG TCT GCC ATC ATG AAT GAG CAG ATT ACG GGC AGG GAC GAC CCA
 asp met leu ser glu leu ser ala ile met asn glu gln ile thr gly arg asp asp pro

7/95

6432/2201	6462/2211
GCA AAG TGC GGA GTG GAG CGA CCC TAC ACC	ACA CGT GTA ACT AGC AAG GGG ACC GCG GCT
ala lys cys gly val glu arg pro tyr thr	thr arg val thr ser lys gly thr ala ala
6492/2221	6522/2231
GTA CCT GTG GTC TCC ATC TCA TCC AGT GCG	GAG GTT TGA GAG GAA CCC TGG AGC ATC CGA
val pro val val ser ile ser ser ser ala	glu val OPA
6552/2241	6582/2251
TGC ACC TCT CAG AGA ACT CTC TAA ATG TTT	TGC AGC TAA TCT CGG GGA AGA AAA AGA TAG
6612/2261	6642/2271
ATT TAA TTT ATT TGA AGT TTT TAC AGT GTT	AAT CTT GTT TAC CTT GCT AGC TTG GGA ATT
6672/2281	6702/2291
TTG CCA GCC TCT GAA TTT GCA CAT TTT CTA	TGA TTC CTT TGT TTC CTT GAA GTA GTA TTG
6732/2301	6762/2311
ATC AAG CCA CGC TAA ACA TTT GTT CTG AAA	TTC CAA TGA ACG TGC AGC TTA AAA GCA AAC
6792/2321	6822/2331
TGA GTT TGC TCT TGG GTG TAA TTT GTT CAA	TTC CAG GTC CTT GTA CAC GCA TTT TAG AGG
6852/2341	6882/2351
TCA AAG TGA ATG TTT TTA TAA CAT TTA AGC	ATA TTT CCA ATG TAA ATA GAA GAT TGT AAA
6912/2361	6942/2371
ATA TAT GGT TTT TAT CAC ATT TCA AAG AAT	GTT TTT AGT TGA TAC TTA TGA AAG TAC CAA
6972/2381	7002/2391
AAT TAT ATG GGT AAC GTT TCA GAT CTT ATA	TTA AAA TAT TTG TGT ATG TGT AAA AAC TGT
7032/2401	7062/2411
TCG ATA AAT ACT AAT CTC TAA AGT TTG TGG	ACT ACC TTT ATT TGT AAT ATA TGT GCT TTT
7092/2421	7122/2431
AAG AGC AAT GGG ATG TGA AAT TAC AAA AAG	TAT TTT GCT GTT GAT AAT ATG AAT ATG AAT
7152/2441	
AAA AAC	

B. Mouse CLASP-2 cDNA sequence

1/1	31/11
CCA CTC GAC TAT GAA AAT GTC ATC GTG CAG	AAG AAG ACG CAG ATC CTA AAC GAC TGC CTG
pro leu asp tyr glu asn val ile val gln	lys lys thr gln ile leu asn asp cys leu
61/21	91/31
CGG GAG <u>ATG</u> CTC CTC TTC CCT TAT GAT GAC	TTC CAG ACG GCC ATC CTG AGG CGG CAG GGG
arg glu met leu leu phe pro tyr asp asp	phe gln thr ala ile leu arg arg gln gly
121/41	151/51
CGG TAC TTA CGC TCC ACG GTC CCT GCA AAT	GCA GAG GAG GAA GCA CAG AGC CTG TTT GTC
arg tyr leu arg ser thr val pro ala asn	ala glu glu glu ala gln ser leu phe val
181/61	211/71
ACT GAG TGC ATC AAA ACC TAC AAC TCT GAC	TGG CAT CTT GTG ACC TAT AAA TAT GAA GAT
thr glu cys ile lys thr tyr asn ser asp	trp his leu val thr tyr lys tyr glu asp

241/81	271/91
TAC TCA GGA GAG TTC CGA CAG CTT CCA AAC	AAA GTG CCC AAG CTG GAT AAA CTT CCG GTC
tyr ser gly glu phe arg gln leu pro asn	lys val pro lys leu asp lys leu pro val
301/101	331/111
CAC GTC TAT GAA GTC GAT GAG GAG GCC GAC	AAA GAT GAG GAT GCT GCT TCC CTT GGG TCT
his val tyr glu val asp glu glu ala asp	lys asp glu asp ala ala ser leu gly ser
361/121	391/131
CAG AAG GGC GGG ATC ACC AAG CAT GGC TGG	CTG TAC AAA GGC AAC ATG AAC AGT GCC ATC
gln lys gly gly ile thr lys his gly trp	leu tyr lys gly asn met asn ser ala ile
421/141	451/151
AGC GTG ACG ATG AGG TCA TTC AAG AGG CGG	TTT TTC CAC CTG ATT CAA CTT GGC GAT GGA
ser val thr met arg ser phe lys arg arg	phe phe his leu ile gln leu gly asp gly
481/161	511/171
TCC TAT AAT CTA AAC TTT TAT AAA GAT GAG	AAG ATC TCC AAG GAA CCG AAA GGG TCC ATA
ser tyr asn leu asn phe tyr lys asp glu	lys ile ser lys glu pro lys gly ser ile
541/181	571/191
TTC CTG GAT TCC TGC ATG GGT GTG ATC CAG	AAC AAC AGA GTC AGG CGC TTC GCT TTT GAG
phe leu asp ser cys met gly val ile gln	asn asn arg val arg arg phe ala phe glu
601/201	631/211
CTC AAG ATG CAA GAC AAA AGC AGT TAC CTT	CTG GCG GCA GAC AGC GAG GCA GAG ATG GAG
leu lys met gln asp lys ser ser tyr leu	leu ala ala asp ser glu ala glu met glu
661/221	691/231
GAG TGG GTC ACT GTT CTC AAC AAG ATC CTC	CAG CTC AAC TTT GAA GCC GCA ATG CAA GAA
glu trp val thr val leu asn lys ile leu	gln leu asn phe glu ala ala met gln glu
721/241	751/251
AAG CGA AAC GGG GAC CCT CAT GAA GAT GAC	GAG CAG AGC AAA CTG GAA GGT TCT GGT TCC
lys arg asn gly asp pro his glu asp asp	glu gln ser lys leu glu gly ser gly ser
781/261	811/271
GGT TTG GAC AGC TAC CTG CCT GAA CTT GCC	AAG AGC ACC AGA GAA GCA GAG ATC AAA TTG
gly leu asp ser tyr leu pro glu leu ala	lys ser thr arg glu ala glu ile lys leu
841/281	871/291
AAA AGC GAG AGC AGA GTG AAG CTT TTT TAC	TTG GAC CCA GAT ACC CAG AAA CTT GAC TTC
lys ser glu ser arg val lys leu phe tyr	leu asp pro asp thr gln lys leu asp phe
901/301	931/311
TCA TCC GCT GAA CCA GAA GTG AAG CCC TTT	GAA GAA AAG TTT GGG AAA AGG ATT CTC GTC
ser ser ala glu pro glu val lys pro phe	glu glu lys phe gly lys arg ile leu val
961/321	991/331
AAG TGC AAC GAT TTG TCC TTT AAC CTG CAG	TGC TGT GTC GCA GAG AAT GAG GAA GGA CCC
lys cys asn asp leu ser phe asn leu gln	cys cys val ala glu asn glu glu gly pro
1021/341	1051/351
ACG ACA AAT GTC GAG CCT TTC TTT GTC ACC	CTG TCC CTG TTC GAC ATA AAA TAC AAC CGA
thr thr asn val glu pro phe phe val thr	leu ser leu phe asp ile lys tyr asn arg
1081/361	1111/371
AAG ATT TCT GCT GAC TTC CAC GTG GAC CTG	AAC CAC TTC TCA GTG CGG CAG ATG CTG GCC
lys ile ser ala asp phe his val asp leu	asn his phe ser val arg gln met leu ala
1141/381	1171/391
CCC ACG TCC CCA GCT CTG ATG AAC GGT GGC	CAG AGC CCA CCT GCC TTC CAG GAT GCC CTT
pro thr ser pro ala leu met asn gly gly	gln ser pro pro ala phe gln asp ala leu
1201/401	1231/411
CAT ACA GCC ATG CAG TAT CCG AAG CAG GGA	ATA TTT TCA GTC ACG TGT CCT CAC CCA GAC
his thr ala met gln tyr pro lys gln gly	ile phe ser val thr cys pro his pro asp
1261/421	1291/431
ATA TTT CTT GTG GCC AGA ATT GAG AAG GTC	CTC CAA GGA AGC ATC ACG CAC TGT GCT GAA
ile phe leu val ala arg ile glu lys val	leu gln gly ser ile thr his cys ala glu
1321/441	1351/451
CCG TAT ATG AGA AGC TCA GAC TCT TCT AAG	GTT GCC CAG AAG GTG CTG AAG AAT GCC AAG
pro tyr met arg ser ser asp ser ser lys	val ala gln lys val leu lys asn ala lys

9/95

1381/461	1411/471
CAG GCA TGC CAA AGA CTA GGA CAG TAC AGA	ATG CCA TTC GCC TGG GCA GCA AGG ACG TTG
gln ala cys gln arg leu gly gln tyr arg	met pro phe ala trp ala ala arg thr leu
1441/481	1471/491
TTT AAA GAC ACC TCT GGA AAC CTG GAT AAA	AAC GCC AGA TTT TCT GCC ATC TAC CGG CAA
phe lys asp thr ser gly asn leu asp lys	asn ala arg phe ser ala ile tyr arg gln
1501/501	1531/511
GAC AGC AAT AAG CTT TCA AAT GAT GAC ATG	CTC AAG CTG CTC GCA GAC TTC CGG AAA CCT
asp ser asn lys leu ser asn asp asp met	leu lys leu leu ala asp phe arg lys pro
1561/521	1591/531
GAG AAG ATG GCC AAA CTC CCA GTG ATT TTA	GGC AAT CTA GAC ATT ACA ATT GAC AGT GTT
glu lys met ala lys leu pro val ile leu	gly asn leu asp ile thr ile asp ser val
1621/541	1651/551
TCC TGT GAC TTC CCT AAT TAT CTA AAT TCA	TCA TAC ATT CCC ATG AGG CAA TTT GAA ACC
ser cys asp phe pro asn tyr leu asn ser	ser tyr ile pro met arg gln phe glu thr
1681/561	1711/571
TGC AGT AAA TCT CCA ATC ACT TTT GAA GTA	GAG GAG TTT GTG CCC TGC ATA CCC AAG CAC
cys ser lys ser pro ile thr phe glu val	glu glu phe val pro cys ile pro lys his
1741/581	1771/591
ACC CAG CCT TAT ACA GTC TAC AGC AAT CAC	CTT TAT GTT TAC CCA AAA TAC TTG AAA TAT
thr gln pro tyr thr val tyr ser asn his	leu tyr val tyr pro lys tyr leu lys tyr
1801/601	1831/611
GAC AGC CAG AAG TCG TTT GCC AAG GCC AGA	AAC ATT GCT ATC TGC ATT GAG TTC AAG GAT
asp ser gln lys ser phe ala lys ala arg	asn ile ala ile cys ile glu phe lys asp
1861/621	1891/631
TCT GAT GAA GAA GAC TCT CAA CCC TTG AAG	TGC ATT TAC GGC AGA CCT GGT GGC CCG GTG
ser asp glu glu asp ser gln pro leu lys	cys ile tyr gly arg pro gly gly pro val
1921/641	1951/651
TTC ACG AGA AGT GCC CTT GCC GCG GTC CTA	CAC CAT CAG CAA AAC CCA GAA TTC TAC GAT
phe thr arg ser ala leu ala ala val leu	his his gln gln asn pro glu phe tyr asp
1981/661	2011/671
GAG ATC AAG ATA GAG CTG CCC GCC CAG CTG	CAT GAG AGG CAC CAT TTA CTG TTC ACC TTC
glu ile lys ile glu leu pro ala gln leu	his glu arg his his leu leu phe thr phe
2041/681	2071/691
TTC CAC GTC AGC TGC GAT AAC TCC ACC AAA	GGA AGC ACG AAG AAG AAG GAC GCT GTG GAA
phe his val ser cys asp asn ser thr lys	gly ser thr lys lys lys asp ala val glu
2101/701	2131/711
ACG CAG GTT GGC TTT TCC TGG CTG CCT CTC	CTG AAA GAT GGA AGG GTG TTG ACG AGT GAG
thr gln val gly phe ser trp leu pro leu	leu lys asp gly arg val leu thr ser glu
2161/721	2191/731
CAG CAC ATC CCC GTC TCG GCT AAC CTG CCA	TCT GGC TAC CTC GGC TAC CAG GAG CTC GGC
gln his ile pro val ser ala asn leu pro	ser gly tyr leu gly tyr gln glu leu gly
2221/741	2251/751
ATG GGC AGG CAT TAT GGT CCA GAG GTT AAG	TGG GTG GAA GGA GGC AAG CCA CTG TTG AAG
met gly arg his tyr gly pro glu val lys	trp val glu gly gly lys pro leu leu lys
2281/761	2311/771
ATC TCC ACT CAT CTG GTT TCC ACA GTG TAC	ACT CAG GAT CAA CAT TTA CAT AAT TTT TTC
ile ser thr his leu val ser thr val tyr	thr gln asp gln his leu his asn phe phe
2341/781	2371/791
CAA TAC TGT CAG AAA ACG GAA TCT GGA GCC	CAA GCC TCA GGG AGT GAA CTA GTA AAA TAC
gln tyr cys gln lys thr glu ser gly ala	gln ala ser gly ser glu leu val lys tyr
2401/801	2431/811
CTT AAG AGT CTG CAT GCG ATG GAA GGC CAT	GTG ATG ATC GCC TTC TTG CCG ACC ATT TTA
leu lys ser leu his ala met glu gly his	val met ile ala phe leu pro thr ile leu
2461/821	2491/831
AAT CAG CTA TTC AGA GTC CTC ACA AGA GCC	ACC CAG GAG GAG GTT GCT GTG AAC GTG ACA
asn gln leu phe arg val leu thr arg ala	thr gln glu glu val ala val asn val thr

10/95

2521/841	2551/851
CGG GTC ATT ATT CAT GTG GTT GCC CAG TGC	CAT GAG GAA GGA TTG GAG AGC CAC TTG AGG
arg val ile ile his val val ala gln cys	his glu glu gly leu glu ser his leu arg
2581/861	2611/871
TCA TAT GTT AAG TTT GCC TAT AAG GCT GAG	CCG TAC GTT GCA TCT GAG TAT AAG ACA GTG
ser tyr val lys phe ala tyr lys ala glu	pro tyr val ala ser glu tyr lys thr val
2641/881	2671/891
CAC GAG GAA CTG ACG AAA TCC ATG ACC ACC	ATT CTC AAG CCT TCT GCC GAT TTC CTT ACC
his glu glu leu thr lys ser met thr thr	ile leu lys pro ser ala asp phe leu thr
2701/901	2731/911
AGC AAC AAA CTT CTG AAG TAC TCT TGG TTT	TTC TTT GAT GTG CTG ATA AAG TCC ATG GCT
ser asn lys leu leu lys tyr ser trp phe	phe phe asp val leu ile lys ser met ala
2761/921	2791/931
CAG CAT TTG ATT GAA AAT AAC AAA GTC AAG	TTA CTG CCG AAC CAG AGA TTT CCG GCC TCC
gln his leu ile glu asn asn lys val lys	leu leu arg asn gln arg phe pro ala ser
2821/941	2851/951
TAC CAT CAC GCT GTG GAA ACC GTG GTG AAC	ATG CTG ATG CCA CAT ATC ACC CAG AAA TTT
tyr his his ala val glu thr val val asn	met leu met pro his ile thr gln lys phe
2881/961	2911/971
CGA GAT AAC CCA GAA GCA TCT AAA AAT GCC	AAT CAC AGC CTC GCT GTG TTC ATC AAG AGA
arg asp asn pro glu ala ser lys asn ala	asn his ser leu ala val phe ile lys arg
2941/981	2971/991
TGC TTC ACC TTC ATG GAC AGA GGC TTC GTC	TTC AAG CAG ATC AAC AAC TAC ATC AGT TGC
cys phe thr phe met asp arg gly phe val	phe lys gln ile asn asn tyr ile ser cys
3001/1001	3031/1011
TTT GCT CCC GGG GAC CCC AAG ACT CTC TTT	GAG TAC AAG TTT GAG TTT CTC CGC GTG GTG
phe ala pro gly asp pro lys thr leu phe	glu tyr lys phe glu phe leu arg val val
3061/1021	3091/1031
TGC AAC CAT GAA CAC TAT ATT CCT TTG AAT	TTG CCG ATG CCA TTT GGA AAA GGA AGA ATT
cys asn his glu his tyr ile pro leu asn	leu pro met pro phe gly lys gly arg ile
3121/1041	3151/1051
CAG AGA TAC CAA GAT CTC CAG CTT GAC TAC	TCC TTA ACA GAC GAG TTC TGC AGA AAC CAC
gln arg tyr gln asp leu gln leu asp tyr	ser leu thr asp glu phe cys arg asn his
3181/1061	3211/1071
TTC TTG GTG GGA CTG TTG CTA AGG GAG GTG	GGC ACT GCG CTC CAG GAG TTC CGG GAG GTC
phe leu val gly leu leu leu arg glu val	gly thr ala leu gln glu phe arg glu val
3241/1081	3271/1091
CGA GTC ATC GCC ATC AGC ATG CTC AAG AAC	CTG CTG ATA AAA CAT TCT TTT GAT GAC AGA
arg val ile ala ile ser met leu lys asn	leu leu ile lys his ser phe asp asp arg
3301/1101	3331/1111
TAC AAT TCG AGG AGT CAC CAG GCA AGG ATA	GCC ACT CTC TAC CTG CCT CTG TTT GGT CTG
tyr asn ser arg ser his gln ala arg ile	ala thr leu tyr leu pro leu phe gly leu
3361/1121	3391/1131
CTT ATT GAA AAT GTC CAG CGG ATC AAC GTG	AGG GAT GTG TCA CCC TTT CCT GTG AAC CCG
leu ile glu asn val gln arg ile asn val	arg asp val ser pro phe pro val asn pro
3421/1141	3451/1151
GGC AGT ATC GTG AAG GAC GAA GCC CTG GCT	GTG CCT GCT GGG AAT CCA CTC ATG ACT CCG
gly ser ile val lys asp glu ala leu ala	val pro ala gly asn pro leu met thr pro
3481/1161	3511/1171
CAG AAG GGA AAC ACA CTT GAC CAC AGC CTG	CAC AAA GAC CTC TTG GGC GCC ATC TCT GGC
gln lys gly asn thr leu asp his ser leu	his lys asp leu leu gly ala ile ser gly
3541/1181	3571/1191
ATT GCT TCT CCG TAT ACA GCC TCA ACC CCC	AAC ATC AAC AGC GTG AGA AAT GCC GAC TCA
ile ala ser pro tyr thr ala ser thr pro	asn ile asn ser val arg asn ala asp ser
3601/1201	3631/1211
AGA GGC TCT CTC ATT AGC ACG GAC TCA GGG	AAC AGC CTT CCA GAC AGG AAC CCC GAG AAG
arg gly ser leu ile ser thr asp ser gly	asn ser leu pro asp arg asn pro glu lys

16

Figure 1 (10 of 35)

3661/1221	3691/1231
AGC AAC TCT CTG GAT AAG CAG CAG AGT GGC	ATG CTG GGA AAT TCC GTG GTT CGA TGC GAC
ser asn ser leu asp lys gln gln ser gly	met leu gly asn ser val val arg cys asp
3721/1241	3751/1251
AAA CTG GAC CAG TCT GAG ATC AAG AGC CTG	CTG ATG TGT TTC CTC TAC GTG CTG AAA AGC
lys leu asp gln ser glu ile lys ser leu	leu met cys phe leu tyr val leu lys ser
3781/1261	3811/1271
ATG TCT GAC GAT GCC CTG TTT ACA TAT TGG	AAC AAA GCT TCA ACT GCT GAA TTG ATG GAT
met ser asp asp ala leu phe thr tyr trp	asn lys ala ser thr ala glu leu met asp
3841/1281	3871/1291
TTC TTT ACA ATA TCT GAG GTC TGC CTG CAC	CAG TTC CAG TAC ATG GGG AAG CGA TAC ATA
phe phe thr ile ser glu val cys leu his	gln phe gln tyr met gly lys arg tyr ile
3901/1301	3931/1311
GCC AGG AAC CAG GAG GGG TTG GGA CCC ATA	GGT CAT GAT CGA AAG TCT CAG ACA TTG CCT
ala arg asn gln glu gly leu gly pro ile	gly his asp arg lys ser gln thr leu pro
3961/1321	3991/1331
GTT TCC CGT AAC AGA ACA GGA ATG ATG CAT	GCC AGA TTG CAG CAG CTG GGC AGC CTG GAT
val ser arg asn arg thr gly met met his	ala arg leu gln gln leu gly ser leu asp
4021/1341	4051/1351
AAC TCT GTC ACT TTT AAC CAC AGC TAC GGC	CAC TCA GAG GCA GAT GTC GTT CAC CAG TCG
asn ser val thr phe asn his ser tyr gly	his ser glu ala asp val val his gln ser
4081/1361	4111/1371
CTT CTC GAA GCC AAC ATC GCT ACT GAG GTC	TGC CTC ACA GCG CTG GAC ACC CTC TCT CTC
leu leu glu ala asn ile ala thr glu val	cys leu thr ala leu asp thr leu ser leu
4141/1381	4171/1391
TTC ACA CTG GCT TTT AAG AAC CAG CTC CTA	GCT GAT CAT GGG CAT AAT CCC CTC ATG AAG
phe thr leu ala phe lys asn gln leu leu	ala asp his gly his asn pro leu met lys
4201/1401	4231/1411
AAA GTT TTT GAC GTC TAC CTG TGT TTC CTT	CAA AAA CAC CAG TCA GAA ATG GCT TTA AAA
lys val phe asp val tyr leu cys phe leu	gln lys his gln ser glu met ala leu lys
4261/1421	4291/1431
AAC GTC TTT ACT GCC TTA AGG TCT CTA ATT	TAT AAG TTC CCC TCG GCG TTC TAC GAG GGG
asn val phe thr ala leu arg ser leu ile	tyr lys phe pro ser ala phe tyr glu gly
4321/1441	4351/1451
CGG GCG GAC ATG TGT GCC TCC CTG TGC TAT	GAG GTC CTC AAG TGC TGC AAC TCC AAG CTC
arg ala asp met cys ala ser leu cys tyr	glu val leu lys cys cys asn ser lys leu
4381/1461	4411/1471
AGT TCC ATC CGG ACG GAG GCC TCC CAG CTG	CTC TAC TTC CTG ATG AGG AAC AAC TTC GAC
ser ser ile arg thr glu ala ser gln leu	leu tyr phe leu met arg asn asn phe asp
4441/1481	4471/1491
TAC ACA GGA AAG AAG TCT TTT GTT CGG ACG	CAC TTA CAG GTC ATC ATC TCT GTC AGC CAA
tyr thr gly lys lys ser phe val arg thr	his leu gln val ile ile ser val ser gln
4501/1501	4531/1511
CTG ATT GCA GAT GTG GTT GGC ATT GGA GGA	ACC AGA TTC CAG CAG TCC TTG TCT ATC ATC
leu ile ala asp val val gly ile gly gly	thr arg phe gln gln ser leu ser ile ile
4561/1521	4591/1531
AAC AAC TGT GCC AAC AGC GAC CGG ATC ATC	AAG CAC ACC AGC TTT TCC TCT GAT GTG AAA
asn asn cys ala asn ser asp arg ile ile	lys his thr ser phe ser ser asp val lys
4621/1541	4651/1551
GAT TTG ACT AAG AGG ATC CGC ACA GTC CTG	ATG GCC ACA GCC CAG ATG AAG GAG CAC GAG
asp leu thr lys arg ile arg thr val leu	met ala thr ala gln met lys glu his glu
4681/1561	4711/1571
AAC GAC CCG GAG ATG CTG GTG GAC CTC CAG	TAC AGC CTG GCT AAG TCC TAC GCC AGC ACC
asn asp pro glu met leu val asp leu gln	tyr ser leu ala lys ser tyr ala ser thr
4741/1581	4771/1591
CCT GAG CTC AGG AAG ACG TGG CTA GAC AGT	ATG GCG AGG ATT CAC GTT AAA AAT GGG GAC
pro glu leu arg lys thr trp leu asp ser	met ala arg ile his val lys asn gly asp

12/95

4801/1601	4831/1611
CTC TCA GAG GCG GCA ATG TGC TAT GTC CAC	GTG ACA GCC TTG GTG GCA GAA TAT CTC ACA
leu ser glu ala ala met cys tyr val his	val thr ala leu val ala glu tyr leu thr
4861/1621	4891/1631
CGG AAA GAA GCT GAC CTA GCA CTC CAG CGG	GAA CCA CCT GCC TTC CCC TAC AGC CAT AGC
arg lys glu ala asp leu ala leu gln arg	glu pro pro ala phe pro tyr ser his ser
4921/1641	4951/1651
ACC TGC CAG AGG AAG AGC TGG GGA GGC ATG	TTC AGA CAG GGG TGC ACA GCC TTC AGG GTT
thr cys gln arg lys ser trp gly gly met	phe arg gln gly cys thr ala phe arg val
4981/1661	5011/1671
ATC ACA CCA AAC ATC GAT GAA GAG GCT TCC	ATG ATG GAA GAC GTC GGC ATG CAG GAC GTC
ile thr pro asn ile asp glu glu ala ser	met met glu asp val gly met gln asp val
5041/1681	5071/1691
CAT TTC AAC GAG GAT GTG CTG ATG GAG CTG	CTG GAG CAG TGT GCG GAT GGA CTT TGG AAG
his phe asn glu asp val leu met glu leu	leu glu gln cys ala asp gly leu trp lys
5101/1701	5131/1711
GCG GAG CGC TAC GAG CTG ATC GCT GAC ATC	TAT AAG CTC ATC ATC CCC ATC TAC GAA AAG
ala glu arg tyr glu leu ile ala asp ile	tyr lys leu ile ile pro ile tyr glu lys
5161/1721	5191/1731
CGG AGG GAT TTC GAG AGA CTA GCC CAT CTG	TAT GAC ACG CTG CAC CGC GCA TAC AGC AAA
arg arg asp phe glu arg leu ala his leu	tyr asp thr leu his arg ala tyr ser lys
5221/1741	5251/1751
GTG ACA GAG GTC ATG CAC TCG GGC CGC AGG	CTC CTG GGG ACC TAC TTC CGG GTG GCC TTC
val thr glu val met his ser gly arg arg	leu leu gly thr tyr phe arg val ala phe
5281/1761	5311/1771
TTT GGA CAG GGG TTC TTC GAA GAC GAA GAT	GGG AAG GAA TAC ATC TAC AAA GAG CCC AAG
phe gly gln gly phe phe glu asp glu asp	gly lys glu tyr ile tyr lys glu pro lys
5341/1781	5371/1791
CTC ACG CCT CTG TCA GAG ATT TCT CAG AGA	CTC CTT AAA CTT TAC TCG GAT AAA TTT GGT
leu thr pro leu ser glu ile ser gln arg	leu leu lys leu tyr ser asp lys phe gly
5401/1801	5431/1811
TCC GAA AAT GTC AAA ATG ATA CAG GAT TCT	GGC AAG GTC AAC CCG AAG GAT CTG GAC TCC
ser glu asn val lys met ile gln asp ser	gly lys val asn pro lys asp leu asp ser
5461/1821	5491/1831
AAG TTT GCC TAC ATC CAG GTG ACC CAC GTG	ACC CCA TTC TTT GAC GAA AAG GAG TTA CAA
lys phe ala tyr ile gln val thr his val	thr pro phe phe asp glu lys glu leu gln
5521/1841	5551/1851
GAG AGG AGA ACA GAG TTT GAA CGA TGT CAC	AAC ATC CGG CGC TTC ATG TTT GAG ATG CCC
glu arg arg thr glu phe glu arg cys his	asn ile arg arg phe met phe glu met pro
5581/1861	5611/1871
TTC ACC CAG ACC GGG AAG AGG CAG GGT GGC	GTG GAG GAG CAG TGT AAG CGG CGG ACC ATC
phe thr gln thr gly lys arg gln gly gly	val glu glu gln cys lys arg arg thr ile
5641/1881	5671/1891
CTG ACA GCA ATA CAC TGC TTC CCC TAC GTG	AAG AAG CGG ATC CCT GTC ATG TAC CAG CAC
leu thr ala ile his cys phe pro tyr val	lys lys arg ile pro val met tyr gln his
5701/1901	5731/1911
CAC ACT GAC CTG AAC CCC ATT GAG GTG GCC	ATC GAT GAA ATG AGC AAG AAG GTG GCC GAG
his thr asp leu asn pro ile glu val ala	ile asp glu met ser lys lys val ala glu
5761/1921	5791/1931
CTC CGC CAG CTC TGC TCG TCG GCT GAA GTG	GAT ATG ATC AAA CTG CAG CTC AAA CTG CAG
leu arg gln leu cys ser ser ala glu val	asp met ile lys leu gln leu lys leu gln
5821/1941	5851/1951
GGC AGT GTG AGC GTC CAG GTC AAT GCT GGT	CCG CTA GCA TAT GCC CGA GCC TTC CTC GAT
gly ser val ser val gln val asn ala gly	pro leu ala tyr ala arg ala phe leu asp
5881/1961	5911/1971
GAC ACC AAC ACA AAA AGA TAC CCT GAC AAT	AAG GTG AAA CTG CTG AAG GAA GTT TTC AGG
asp thr asn thr lys arg tyr pro asp asn	lys val lys leu leu lys glu val phe arg

16
Figure X (12 of 35)

13/95

5941/1981	5971/1991
CAA TTT GTG GAA GCT TGT GGT CAA GCC TTG	GCA GTG AAC GAG CGT CTC ATT AAA GAA GAC
gln phe val glu ala cys gly gln ala leu	ala val asn glu arg leu ile lys glu asp
6001/2001	6031/2011
CAA CTG GAG TAC CAG GAA GAG ATG AAG GCC	AAC TAC AGG GAG ATG GCC AAG GAG CTC TCC
gln leu glu tyr gln glu glu met lys ala	asn tyr arg glu met ala lys glu leu ser
6061/2021	6091/2031
GAC ATC ATG CGT GAG CAG ATT TGC CCC CTG	GAG GAG AAG ACA AGC GTG CTA CCA AAT TCC
asp ile met arg glu gln ile cys pro leu	glu glu lys thr ser val leu pro asn ser
6121/2041	6151/2051
CTG CAC ATC TTC AAC GCC ATC AGC GGG ACA	CCA ACA AGC ACA GTG GTT CAA GGG TTG ACC
leu his ile phe asn ala ile ser gly thr	pro thr ser thr val val gln gly leu thr
6181/2061	6211/2071
AGC TCG TCC TCA GTT GTG TGA TTT TAC CTC	ATG AAC CGT GTG TGG GGA CAT GCT TTG TCA
ser ser ser ser val val OPA	
6241/2081	6271/2091
TGT GCA AAC TCA GGA TGA CTT CCA GAG CTA	ATC ACT GGT GTG GCC AAG CAC AGG AAG AAG
6301/2101	6331/2111
CCA TGG GGA ATG GGA GAG AGA AGG AGC CTG	GAC TGT GAT ATT TAA TAG CAG ATT TTA TAG
6361/2121	6391/2131
GAG TCG GGG GAA GGT GCA CAT AGT TTT TTA	AAT CTC ACT GGC AAT ATT TAG TTT TCC TCA
6421/2141	
TGT CTT AAC AGG TAT ATG TGG ATA CTC TTG	

C. Mouse CLASP-3 cDNA sequence

1/1	31/11
GTT TCA GCT GTG CCT GAA GAA AGT GAA ATG	GAC CCA CAT GTT AGA GAT TGT ATA AGA AGT
val ser ala val pro glu glu ser glu met	asp pro his val arg asp cys ile arg ser
61/21	91/31
TAC ACA GAA GAC TGG GCA GTT GTG GTC AGA	AAA TAC CAT AAA CTG GGA ACA GGA TTT AAC
tyr thr glu asp trp ala val val val arg	lys tyr his lys leu gly thr gly phe asn
121/41	151/51
CCC AAC ACA TTG GAT AAG CAG AAA GAA AGG	CAA AAA GGA CTG CCC AGA CAA GTC TTT GAA
pro asn thr leu asp lys gln lys glu arg	gln lys gly leu pro arg gln val phe glu
181/61	211/71
TCT GAT GAA GCT CCC GAT GGC AGC AGC TAC	CAG GAT GAG CAA GAT GAT CTT AAA AGA CGT
ser asp glu ala pro asp gly ser ser tyr	gln asp glu gln asp asp leu lys arg arg
241/81	271/91
TCG ATG TCA ATA GAT GAT ACT CCA AGG GGT	AGC TGG GCC TGC AGT ATC TTT GAC TTA AAA
ser met ser ile asp asp thr pro arg gly	ser trp ala cys ser ile phe asp leu lys
301/101	331/111
AAT TCA CTT CCT GAT GCC TTG CTT CCT AAT	TTA CTT GAT CGA ACT CCA AAT GAA GAA ATA
asn ser leu pro asp ala leu leu pro asn	leu leu asp arg thr pro asn glu glu ile
361/121	391/131
GAC CAT CAG AAT GAT GAC CAA AGG AAA TCA	AAC CGC CAC AAG GAA CTG TTT GCT TTG CAT
asp his gln asn asp asp gln arg lys ser	asn arg his lys glu leu phe ala leu his
421/141	451/151
CCA TCA CCA GAT GAG GAA GAA CCA ATC GAA	AGG CTC AGT GTT CCT GAT GTG CCC AAA GAG
pro ser pro asp glu glu glu pro ile glu	arg leu ser val pro asp val pro lys glu
481/161	511/171
CAT TTC GGA CAA AGA CTT CTT GTG AAA TGT	TTA TCA CTC AAG TTT GAG ATT GAA ATT GAG
his phe gly gln arg leu leu val lys cys	leu ser leu lys phe glu ile glu ile glu

14/95

541/181	571/191
CCC ATT TTT GCA AGT TTG GCT TTA TAT GAT	GTC AAG GAG AAG AAA AAG ATT TCC GAG AAT
pro ile phe ala ser leu ala leu tyr asp	val lys glu lys lys lys ile ser glu asn
601/201	631/211
TTT TAT TTC GAC CTT AAT TCA GAG CAG ATG	AAG GGA CTG TTA CGA CCG CAT GTG CCC CCT
phe tyr phe asp leu asn ser glu gln met	lys gly leu leu arg pro his val pro pro
661/221	691/231
GCT GCC ATC ACC ACT CTG GCA AGA TCA GCC	ATT TTT TCT ATA ACT TAT CCT TCC CAA GAT
ala ala ile thr thr leu ala arg ser ala	ile phe ser ile thr tyr pro ser gln asp
721/241	751/251
GTC TTT CTT GTG ATA AAG TTA GAA AAA GTC	CTT CAG CAA GGA GAC ATT GGA GAG TGT GCA
val phe leu val ile lys leu glu lys val	leu gln gln gly asp ile gly glu cys ala
781/261	811/271
GAA CCA TAT ATG ATT TTC AAA GAA GCT GAT	GCC ACC AAG AAT AAG GAA AAA TTG GAG AAA
glu pro tyr met ile phe lys glu ala asp	ala thr lys asn lys glu lys leu glu lys
841/281	871/291
TTG AAA AGT CAA GCT GAC CAA TTT TGC CAG	AGA CTT GGG AAA TAC CGC ATG CCT TTT GCT
leu lys ser gln ala asp gln phe cys gln	arg leu gly lys tyr arg met pro phe ala
901/301	931/311
TGG ACT GCG ATT CAT TTA ATG AAT ATT GTT	AGC AGT GCT GGC AGC TTA GAA AGA GAC TCC
trp thr ala ile his leu met asn ile val	ser ser ala gly ser leu glu arg asp ser
961/321	991/331
ACA GAA GTC GAG ATC AGT ACT GGA GAA CGG	AAA GGT TCT TGG TCA GAG AGG AGG AAT TCT
thr glu val glu ile ser thr gly glu arg	lys gly ser trp ser glu arg arg asn ser
1021/341	1051/351
AGT CTT GTT GGC AGG CGG TCC CTG GAG AGG	ACG ACC AGT GGG GAT GAT GCT TGC AAC TTG
ser leu val gly arg arg ser leu glu arg	thr thr ser gly asp asp ala cys asn leu
1081/361	1111/371
ACC AGC TTC TGG CCT GCC ACC CTC ACT GTG	GCA AAC TTT TTT AAG CAG GAA GGA GAC CGT
thr ser phe trp pro ala thr leu thr val	ala asn phe phe lys gln glu gly asp arg
1141/381	1171/391
TTA AGT GAT GAG GAC CTG TAC AAG TTC CTC	GCT GAT ATG AGA AGG CCG TCT TCT GTC TTA
leu ser asp glu asp leu tyr lys phe leu	ala asp met arg arg pro ser ser val leu
1201/401	1231/411
CGG AGG CTG AGA CCA ATT ACA GCT CAG CTG	AAG ATA GAC ATT TCT CCT GCA CCT GAA AAT
arg arg leu arg pro ile thr ala gln leu	lys ile asp ile ser pro ala pro glu asn
1261/421	1291/431
CCC CAT TAC TGC CTA ACC CCA GAG CTG CTT	CAG GTG AAG CTG TAC CCC GAC AGC CGA GTC
pro his tyr cys leu thr pro glu leu leu	gln val lys leu tyr pro asp ser arg val
1321/441	1351/451
AGG CCC ACC AGA GAA ATT TTA GAA TTT CCT	GCC AGG GAT GTC TAT GTT CCA AAC ACA ACT
arg pro thr arg glu ile leu glu phe pro	ala arg asp val tyr val pro asn thr thr
1381/461	1411/471
TAC AGA AAT CTT CTC TAC ATT TAC CCT CAA	AGT CTT AAT TTT GCC AAC CGT CAA GGT TCT
tyr arg asn leu leu tyr ile tyr pro gln	ser leu asn phe ala asn arg gln gly ser
1441/481	1471/491
GCC AGA AAC ATC ACA GTG AAA GTC CAG TTT	ATG TAT GGG GAA GAC CCG AGC AAC GCA ATG
ala arg asn ile thr val lys val gln phe	met tyr gly glu asp pro ser asn ala met
1501/501	1531/511
CCG GTA ATC TTT GGT AAA TCT AGC TGT TCA	GAA TTT TCA AAG GAA GCC TAT ACA GCC GTA
pro val ile phe gly lys ser ser cys ser	glu phe ser lys glu ala tyr thr ala val
1561/521	1591/531
GTA TAT CAT AAC AGG TCT CCT GAT TTT CAC	GAG GAA ATC AAA GTC AAG CTC CCC GCC ACG
val tyr his asn arg ser pro asp phe his	glu glu ile lys val lys leu pro ala thr
1621/541	1651/551
CTA ACT GAC CAC CAC CAC TTG CTC TTT ACT	TTT TAT CAT GTT AGT TGC CAG CAG AAA CAA
leu thr asp his his his leu leu phe thr	phe tyr his val ser cys gln gln lys gln

16

Figure X (14 of 35)

15/95

1681/561	1711/571
AAC ACT CCT CTC GAA ACC CCA GTC GGA TAT	ACA TGG ATA CCA ATG CTG CAG AAT GGA CGG
asn thr pro leu glu thr pro val gly tyr	thr trp ile pro met leu gln asn gly arg
1741/581	1771/591
TTG AAG ACA GGG CAG TTC TGC CTG CCA GTC	TCC CTG GAA AAA CCA CCG CAG GCT TAT TCA
leu lys thr gly gln phe cys leu pro val	ser leu glu lys pro pro gln ala tyr ser
1801/601	1831/611
GTG CTT TCC CCC GAG GTC CCT CTA CCT GGT	ATG AAG TGG GTG GAC AAC CAC AAA GGA GTA
val leu ser pro glu val pro leu pro gly	met lys trp val asp asn his lys gly val
1861/621	1891/631
TTT AAT GTT GAA GTT GTT GCT GTT TCA TCC	ATT CAT ACA CAA GAC CCT TAT CTA GAC AAA
phe asn val glu val val ala val ser ser	ile his thr gln asp pro tyr leu asp lys
1921/641	1951/651
TTC TTT GCT CTT GTC AAT GCT CTG GAT GAA	CAC ATG TTC CCG GTC CGA ATT GGG GAC ATG
phe phe ala leu val asn ala leu asp glu	his met phe pro val arg ile gly asp met
1981/661	2011/671
TGG ATC ATG GAA AAC AAC TTA GAG AGT GAA	CTG AAG AGC AGC ATT TCA GCC TTG AAT TCC
trp ile met glu asn asn leu glu ser glu	leu lys ser ser ile ser ala leu asn ser
2041/681	2071/691
TCA CAG CTG GAA CCC GTA GTC CGG TTT CTT	CAT CTT CTG CTT GAT AAA CTC ATA CTT TTA
ser gln leu glu pro val val arg phe leu	his leu leu leu asp lys leu ile leu leu
2101/701	2131/711
GTT GTT AGA CCA CCT GTG ATT GCT GGC CAA	ATA GTT AAT CTA GGG CAA GCA TCT TTT GAA
val val arg pro pro val ile ala gly gln	ile val asn leu gly gln ala ser phe glu
2161/721	2191/731
GCT ATG GCG TCA ATT ATA AAT CGA CTT CAC	AAA AAC TTA GAA GGA AAT CAT GAC CAG CAT
ala met ala ser ile ile asn arg leu his	lys asn leu glu gly asn his asp gln his
2221/741	2251/751
GGC AGA AAC AAC CTT CTC GCA TCG TAT ATC	TAT TAT GTG TTC CGC CTG CCA AAT ACT TAC
gly arg asn asn leu leu ala ser tyr ile	tyr tyr val phe arg leu pro asn thr tyr
2281/761	2311/771
CCT AAT TCA CCG TCA CCA GGT CCC GGG GGT	TTG GGA GGA TCA GTG CAT TAT GCC ACA ATG
pro asn ser pro ser pro gly pro gly gly	leu gly gly ser val his tyr ala thr met
2341/781	2371/791
GCT AGG TCT GCA GTG AGA CCT GCG AGC CTT	AAC TTA AAT CGG TCT CGA AGC CTT AGC AAC
ala arg ser ala val arg pro ala ser leu	asn leu asn arg ser arg ser leu ser asn
2401/801	2431/811
AGT AAC CCA GAT ATA TCT GGG ACT CCC ACA	TCA CCA GAT GAT GAA GTT CGG TCA ATC ATT
ser asn pro asp ile ser gly thr pro thr	ser pro asp asp glu val arg ser ile ile
2461/821	2491/831
GGC AGT AAG GCT ATG GAT CGA AGT TGT AAT	CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT
gly ser lys ala met asp arg ser cys asn	arg met ser ser his thr glu thr ser ser
2521/841	2551/851
TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA	ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT
phe leu gln thr leu thr gly arg leu pro	thr lys lys leu phe his glu glu leu ala
2581/861	2611/871
TTG CAG TGG GTC GTT TGC AGT GGC AGC GTT	CGG GAG TCG GCT TTG CAG CAA GCC TGG TTC
leu gln trp val val cys ser gly ser val	arg glu ser ala leu gln gln ala trp phe
2641/881	2671/891
TTT TTT GAG TTG ATG GTA AAG AGC ATG GTG	CAC CAC TTG TAC TTT AAT GAT AAG CTC GAC
phe phe glu leu met val lys ser met val	his his leu tyr phe asn asp lys leu asp
2701/901	2731/911
GCT CCG AGG AAA AGT CGC TTT CCA GAA CGT	TTT ATG GAT GAT ATT GCT GCC CTG GTT AGC
ala pro arg lys ser arg phe pro glu arg	phe met asp asp ile ala ala leu val ser
2761/921	2791/931
ACA ATT GCT GGC GAT GTC GTG TCG CGG TTT	CAG AAG GAT ACA GAA ATG GTT GAG AGA CTC
thr ile ala gly asp val val ser arg phe	gln lys asp thr glu met val glu arg leu

16
Figure X (15 of 35)

2821/941	2851/951
AAC ACA AGC CTT GCC TTC TTT CTC AAT GAC	CTG CTG TCA GTT ATG GAC AGG GGG TTT GTT
asn thr ser leu ala phe phe leu asn asp	leu leu ser val met asp arg gly phe val
2881/961	2911/971
TTT AGC CTC ATA AAG TCC TGC TAC AAA CAG	GTA TCA GCA AAG CTG TAT TCA CTG CCA AAT
phe ser leu ile lys ser cys tyr lys gln	val ser ala lys leu tyr ser leu pro asn
2941/981	2971/991
CCA AGT GTC CTG GTG TCC CTG AGG TTG GAC	TTT TTG CGA ATC ATC TGC AGC CAT GAG CAC
pro ser val leu val ser leu arg leu asp	phe leu arg ile ile cys ser his glu his
3001/1001	3031/1011
TAT GTT ACA TTA AAC TTA CCC TGC AGC TTG	CTC ACC CCG CCT GCA TCT CCA TCA CCT TCT
tyr val thr leu asn leu pro cys ser leu	leu thr pro pro ala ser pro ser pro ser
3061/1021	3091/1031
GTT TCT TCT GCA ACA TCT CAG AGC TCT GGA	TTC TCC ACC AGT GTG CAG GAC CAG AAG ATT
val ser ser ala thr ser gln ser ser gly	phe ser thr ser val gln asp gln lys ile
3121/1041	3151/1051
GCA AAC ATG TTC GAA TTG TCC TTA CCC TTC	CGC CAG CAG CAT TAC CTG GCA GGC CTC GTG
ala asn met phe glu leu ser leu pro phe	arg gln gln his tyr leu ala gly leu val
3181/1061	3211/1071
CTG ACT GAG CTT GCA CTC ATT CTA GAC CCT	GAC GCT GAA GGA CTG TTT GGA TTG CAT AAG
leu thr glu leu ala leu ile leu asp pro	asp ala glu gly leu phe gly leu his lys
3241/1081	3271/1091
AAA GTC ATC AAT ATG GTA CAC AAC TTA CTG	TCC ACT CAC GAC TCT GAC CCA CGG TAC TCT
lys val ile asn met val his asn leu leu	ser thr his asp ser asp pro arg tyr ser
3301/1101	3331/1111
GAC CCT CAG ATA AAA GCT CGG GTG GCT ATG	TTG TAC CTA CCT CTT ATT GGT ATT ATC ATG
asp pro gln ile lys ala arg val ala met	leu tyr leu pro leu ile gly ile ile met
3361/1121	3391/1131
GAA ACT GTA CCT CAA CTG TAT GAT TTT ACA	GAA TCA CAC AAT CAA CGA GGA AGG CCA ATT
glu thr val pro gln leu tyr asp phe thr	glu ser his asn gln arg gly arg pro ile
3421/1141	3451/1151
TGT ATA GCC CCT GAT GAC TAT GAC AGT GAG	AGT GGG AGC ATG ATA AGC CAG ACG GTT GCC
cys ile ala pro asp asp tyr asp ser glu	ser gly ser met ile ser gln thr val ala
3481/1161	3511/1171
ATG GCA ATT GCA GGA ACA TCC GTC CCT CAG	CTG ACA AGA CCT GGC AGT TTT CTC CTC ACG
met ala ile ala gly thr ser val pro gln	leu thr arg pro gly ser phe leu leu thr
3541/1181	3571/1191
TCA ACG AGT GGC CGG CAG CAC ACC ACC TTC	TCA GCA GAG TCA AGC AGG AGC CTT TTG ATC
ser thr ser gly arg gln his thr thr phe	ser ala glu ser ser arg ser leu leu ile
3601/1201	3631/1211
TGT CTG CTT TGG GTT CTC AAG AAT GCA GAT	GAA ACG GTT CTG CAG AAA TGG TTT ACA GAT
cys leu leu trp val leu lys asn ala asp	glu thr val leu gln lys trp phe thr asp
3661/1221	3691/1231
CTC TCA GTC CTC CAG CTG AAC CGG TTG TTA	GAT CTG CTT TAC CTG TGT GTA TCT TGC TTT
leu ser val leu gln leu asn arg leu leu	asp leu leu tyr leu cys val ser cys phe
3721/1241	3751/1251
GAG TAC AAA GGA AAA AAG GTA TTT GAA CGA	ATG AAT AGT TTA ACT TTT AAG AAA TCA AAA
glu tyr lys gly lys lys val phe glu arg	met asn ser leu thr phe lys lys ser lys
3781/1261	3811/1271
GAC ATG AGA GCC AAG CTT GAA GAA GCC ATT	CTG GGG AGC ATC GGT GCC AGG CAG GAA ATG
asp met arg ala lys leu glu glu ala ile	leu gly ser ile gly ala arg gln glu met
3841/1281	3871/1291
GTA CGG CGG AGC CGA GGG CAG CTC GAG AGG	AGC CCA TCT GGA AGC GCC TTT GGG AGC CAA
val arg arg ser arg gly gln leu glu arg	ser pro ser gly ser ala phe gly ser gln
3901/1301	3931/1311
GAA AAC CTG CGG TGG AGA AAG GAC ATG ACT	CAC TGG CGT CAG AAC TCA GAG AAA CTC GAT
glu asn leu arg trp arg lys asp met thr	his trp arg gln asn ser glu lys leu asp

3961/1321
 AAG TCA AGA GCA GAG ATA GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACT GAA GCA
 lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu ala
 4021/1341
 AAC CTC ATC ATC TTA GAC ACG CTA GAG ATC ATC GTC CAG ACT GTG TCT GTA ACG GAA TCC
 asn leu ile ile leu asp thr leu glu ile ile val gln thr val ser val thr glu ser
 4081/1361
 AAA GAG AGT ATC CTG GGT GGT GTG CTA AAA GTG CTG CTA CAG AGC ATG GCC TGC AAC CAA
 lys glu ser ile leu gly gly val leu lys val leu leu gln ser met ala cys asn gln
 4141/1381
 AGT GCA GTC TAT CTG CAG CAC TGC TTC GCC ACG CAG AGA GCC CTG GTC TCA AAG TTT CCT
 ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe pro
 4201/1401
 GAG CTC TTG TTT GAG GAA GAG ACA GAG CAG TGT GCG GAT CTG TGC CTC CGG CTT CTC CGT
 glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu arg
 4261/1421
 CAT TGC AGT AGC AGC ATC AGT ACA ATC CGG TCG CAC GCT AGT GCC TCC CTT TAC CTC CTC
 his cys ser ser ser ile ser thr ile arg ser his ala ser ala ser leu tyr leu leu
 4321/1441
 ATG AGG CAG AAC TTT GAG ATC GGG AAT AAC TTT GCC AGA GTG AAA ATG CAA GTG ACG ATG
 met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val thr met
 4381/1461
 TCA CTG TCC TCT TTG GTG GGT ACG TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGC TCT
 ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg ser
 4441/1481
 CTA AAA ACT ATT TTG ACA TAT GCT GAA GAA GAT CTA GAA TTG AGG GAA ACC ACA TTT CCT
 leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe pro
 4501/1501
 GAT CAG GTC CAA GAT TTG GTC TTC AAT CTC CAT ATG ATC CTT TCT GAC ACT GTT AAG ATG
 asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys met
 4561/1521
 AAG GAG CAT CAG GAA GAC CCA GAA ATG CTG ATT GAT CTC ATG TAC AGA ATC GCC AAG GGC
 lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys gly
 4621/1541
 TAC CAG ACG TCT CCA GAC CTG CGC CTG ACC TGG TTG CAG AAC ATG GCT GGC AAG CAC TCT
 tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his ser
 4681/1561
 GAA CGA AGC AAT CAT GCC GAA GCT GCT CAG TGC CTG GTC CAC TCC GCA GCC CTT GTC GCC
 glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val ala
 4741/1581
 GAG TAT CTG AGC ATG CTG GAA GAT CGG AAG TAT CTT CCT GTT GGA TGC GTA ACA TTC CAG
 glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe gln
 4801/1601
 AAT ATT TCA TCT AAT GTA TTG GAA GAA TCT GCT GTC TCA GAT GAT GTG GTA TCT CCA GAT
 asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro asp
 4861/1621
 GAA GAA GGC ATT TGC TCT GGA AAG TAC TTC ACT GAA TCG GGA CTG GTG GGC TTA CTG GAA
 glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu glu
 4921/1641
 CAA GCG GCT GCT TCC TTC TCC ATG GCG GGC ATG TAC GAA GCA GTT AAT GAG GTT TAC AAA
 gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr lys
 4981/1661
 GTA CTC ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAG CTC TCC ACA ATT CAT GGC
 val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his gly
 5041/1681
 AAA CTT CAG GAG GCA TTC AGC AAA ATC GTC CAT CAG GAT GGT AAG CGG ATG TTT GGC ACC
 lys leu gln glu ala phe ser lys ile val his gln asp gly lys arg met phe gly thr

18/95

5101/1701	5131/1711
TAT TTC CGT GTT GGT TTT TAT GGA ACC AAG	TTC GGG GAT TTG GAT GAA CAG GAA TTT GTT
tyr phe arg val gly phe tyr gly thr lys	phe gly asp leu asp glu gln glu phe val
5161/1721	5191/1731
TAC AAG GAG CCT GCA ATA ACC AAA CTC GCA	GAG ATT TCT CAC AGA TTG GAG GGA TTT TAT
tyr lys glu pro ala ile thr lys leu ala	glu ile ser his arg leu glu gly phe tyr
5221/1741	5251/1751
GGA GAA AGA TTT GGA GAG GAT GTG CTT GAA	GTA ATC AAG GAC TCT AAT CCT GTA GAC AAG
gly glu arg phe gly glu asp val leu glu	val ile lys asp ser asn pro val asp lys
5281/1761	5311/1771
TGC AAA TTA GAT CCA AAC AAG GCA TAT ATT	CAG ATT ACC TAC GTG GAG CCC TTC TTT GAC
cys lys leu asp pro asn lys ala tyr ile	gln ile thr tyr val glu pro phe phe asp
5341/1781	5371/1791
ACC TAT GAG ATG AAG GAC AGA ATC ACT TAT	TTT GAC AAA AAT TAT AAT CTC CGG CGT TTC
thr tyr glu met lys asp arg ile thr tyr	phe asp lys asn tyr asn leu arg arg phe
5401/1801	5431/1811
ATG TAC TGC ACA CCC TTC ACT TTA GAT GGC	CGT GCT CAT GGG GAG CTT CAT GAA CAA TTC
met tyr cys thr pro phe thr leu asp gly	arg ala his gly glu leu his glu gln phe
5461/1821	5491/1831
AAA CGG AAG ACC ATT CTG ACA ACG TCT CAT	GCC TTT CCT TAC ATT AAA ACA AGA GTC AAT
lys arg lys thr ile leu thr thr ser his	ala phe pro tyr ile lys thr arg val asn
5521/1841	5551/1851
GTC ACT CAC AAA GAA GAG ATA ATC TTA ACA	CCA ATT GAA GTT GCT ATC GAA GAC ATG CAG
val thr his lys glu glu ile ile leu thr	pro ile glu val ala ile glu asp met gln
5581/1861	5611/1871
AAA AAG ACT CAG GAA TTG GCA TTT GCA ACA	CAT CAG GAT CCA GCA GAC CCC AAA ATG CTT
lys lys thr gln glu leu ala phe ala thr	his gln asp pro ala asp pro lys met leu
5641/1881	5671/1891
CAA ATG GTC CTC CAG GGG TCT GTA GGA ACA	ACT GTA AAC CAG GGA CCT CTG GAG GTT GCC
gln met val leu gln gly ser val gly thr	thr val asn gln gly pro leu glu val ala
5701/1901	5731/1911
CAG GTC TTC CTG TCT GAA ATA CCT GGT GAC	CCG AAG CTC TTC AGA CAT CAC AAC AAG CTG
gln val phe leu ser glu ile pro gly asp	pro lys leu phe arg his his asn lys leu
5761/1921	5791/1931
CGC CTT TGT TTC AAG GAC TTT ACT AAA AGG	TGT GAG GAT GCC TTA CGA AAA AAT AAG AGC
arg leu cys phe lys asp phe thr lys arg	cys glu asp ala leu arg lys asn lys ser
5821/1941	5851/1951
TTA ATT GGA CCA GAT CAA AAG GAG TAT CAA	AGA GAA CTG GAG AGA AAT TAC CAT CGC CTT
leu ile gly pro asp gln lys glu tyr gln	arg glu leu glu arg asn tyr his arg leu
5881/1961	5911/1971
AAA GAG GCT CTG CAG CCA CTG ATA AAC AGA	AAA ATC CCT CAG CTA TAC AAG GCT GTG TTG
lys glu ala leu gln pro leu ile asn arg	lys ile pro gln leu tyr lys ala val leu
5941/1981	5971/1991
CCT GTC ACT TGC CAC AGA GAT TCC TTC AGC	CGA ATG AGC CTT CGA AAA ATG GAA CTC TAA
pro val thr cys his arg asp ser phe ser	arg met ser leu arg lys met glu leu OCH
6001/2001	6031/2011
AAT ACA CAC TTG TTC TAT TCA TTT GAA AAG	AAC CAT GTA TTC AAC ACT GAG TGT GAG GTC
6061/2021	6091/2031
TAT TGA AAA ATA GGA CTT GGA TGT CAT TCT	GGA AGC AAT AGT ATC GAT TTA CTC TCT GAA
6121/2041	6151/2051
GAA TGT GCT CCC AGA TGC AGG CTG TTA CGT	GTG AGG CTT GTG GCG TGG TTT CTA ACC TTC
6181/2061	6211/2071
TGG TAA CAT GCT GTC ATC TTA AAA ACA AAA	GGT TTT AAT GAT TCA

19/95

D. Mouse CLASP-4 cDNA sequence

-150

AGAAGAAAGAGCCGCGGGAGCTGGGCGCGGGGCGGGCGAGCTGAGATGTGGCCGGCCCGTCGGCGTGTAACACAGGCAGC
AGCAGCAGCAGCGCGCCCGCGGGCCCGGGGCACTGAGCGCTCCGCGCCGAGACCTGCCCGCCACCTCTGCC -1

1/1	31/11
ATG GCC GAA GTG CGC AAA TTC ACC AAG CGG	CTG AGC AAG CCA GGC ACG GCA GCC GAG CTC
Met ala glu val arg lys phe thr lys arg	leu ser lys pro gly thr ala ala glu leu
61/21	91/31
CGC CAG AGC GTG TCG GAG GCC GTG CGG GGC	TCC GTG GTG CTG GAA AAG GCC AAG TTA GTT
arg gln ser val ser glu ala val arg gly	ser val val leu glu lys ala lys leu val
121/41	151/51
GAA CCC CTG GAC TAT GAA AAT GTT ATC ACT	CAA CGG AAA ACC CAG ATC TAC AGT GAT CCC
glu pro leu asp tyr glu asn val ile thr	gln arg lys thr gln ile tyr ser asp pro
181/61	211/71
CTC AGA GAT CTG CTT ATG TTC CCC ATG GAA	GAC ATA TCT ATC TCA GTG ATT GGT CGT CAG
leu arg asp leu leu met phe pro met glu	asp ile ser ile ser val ile gly arg gln
241/81	271/91
CGC AGA ACA GTG CAG TCT ACT GTA CCA GAG	GAT GCT GAA AAG AGG GCC CAG AGT TTA TTT
arg arg thr val gln ser thr val pro glu	asp ala glu lys arg ala gln ser leu phe
301/101	331/111
GTC AAA GAG TGT ATT AAG ACC TAC AGC ACA	GAT TGG CAT GTG GTG AAC TAT AAG TAT GAG
val lys glu cys ile lys thr tyr ser thr	asp trp his val val asn tyr lys tyr glu
361/121	391/131
GAT TTC TCT GGG GAC TTT CGG ATG TTG CCA	TGC AAG TCT TTG AGA CCT GAA AAG ATT CCT
asp phe ser gly asp phe arg met leu pro	cys lys ser leu arg pro glu lys ile pro
421/141	451/151
AAT CAT GTG TTT GAG ATT GAT GAA GAT TGC	GAG AAA GAT GAG GAT TCA TCT TCT TTA TGT
asn his val phe glu ile asp glu asp cys	glu lys asp glu asp ser ser ser leu cys
481/161	511/171
TCT CAG AAG GGT GGT GTG ATA AAA CAA GGT	TGG TTG CAT AAA GCA AAT GTA AAT AGC ACC
ser gln lys gly gly val ile lys gln gly	trp leu his lys ala asn val asn ser thr
541/181	571/191
ATC ACA GTA ACC ATG AAG GTG TTC AAG AGA	CGG TAT TTT TAT TTG ACT CAA CTT CCT GAT
ile thr val thr met lys val phe lys arg	arg tyr phe tyr leu thr gln leu pro asp
601/201	631/211
GGT TCA TAT ATT CTC AAT TCT TAT AAA GAT	GAG AAA AAT TCC AAA GAG TCT AAA GGT TGC
gly ser tyr ile leu asn ser tyr lys asp	glu lys asn ser lys glu ser lys gly cys
661/221	691/231
ATC TAC TTG GAT GCC TGC ATT GAT GTT GTT	CAG TGC CCC AAA ATG CGC CGT CAT GCT TTT
ile tyr leu asp ala cys ile asp val val	gln cys pro lys met arg arg his ala phe
721/241	751/251
GAA CTC AAG ATG TTA GAT AAG TAT AGC CAT	TAT CTG GCA GCT GAA ACG GAG CAG GAA ATG
glu leu lys met leu asp lys tyr ser his	tyr leu ala ala glu thr glu gln glu met
781/261	811/271
GAG GAA TGG TTG ATA ATG TTG AAA AAG ATT	ATT CAG ATC AAT ACT GAC AGT TTA GTG CAA
glu glu trp leu ile met leu lys lys ile	ile gln ile asn thr asp ser leu val gln
841/281	871/291
GAG AAA AAG GAC ACA GTC GAG GCA ATA CAA	GAG GAG GAA ACT AGC AGC CAA GGA AAA GCC
glu lys lys asp thr val glu ala ile gln	glu glu glu thr ser ser gln gly lys ala
901/301	931/311
GAG AAC ATC ATG GCC AGT TTG GAA AGG AGC	ATG CAT CCG GAA CTG ATG AAG TAT GGC AGA
glu asn ile met ala ser leu glu arg ser	met his pro glu leu met lys tyr gly arg

16
Figure 1 (19 of 35)

20/95

961/321	991/331
GAA ACA GAA CAA CTG AAC AAA CTC AGT AGA	GGA GAC GGA AGA CAG AAT CTC TTT TCT TTC
glu thr glu gln leu asn lys leu ser arg	gly asp gly arg gln asn leu phe ser phe
1021/341	1051/351
GAC TCA GAG GTT CAG AGA TTA GAC TTT TCA	GGA ATT GAG CCT GAT GTA AAG CCA TTT GAA
asp ser glu val gln arg leu asp phe ser	gly ile glu pro asp val lys pro phe glu
1081/361	1111/371
GAA AAG TGC AAC AAG CGT TTC ATG GTG AAT	TGC CAT GAT TTA ACT TTC AAT ATC TTG GGT
glu lys cys asn lys arg phe met val asn	cys his asp leu thr phe asn ile leu gly
1141/381	1171/391
CAC ATT GGA GAC AAT GCA AAA GGA CCA CCC	ACA AAT GTT GAG CCC TTT TTC ATC AAC CTC
his ile gly asp asn ala lys gly pro pro	thr asn val glu pro phe phe ile asn leu
1201/401	1231/411
GCC TTA TTT GAT GTA AAG AAC AAT TGT AAA	ATT TCA GCA GAC TTT CAT GTA GAT TTG AAC
ala leu phe asp val lys asn asn cys lys	ile ser ala asp phe his val asp leu asn
1261/421	1291/431
CCA CCC TCT GTC CGT GAA ATG CTG TGG GGT	ACC TCG ACC CAA CTG TCC AAT GAT GGG AAT
pro pro ser val arg glu met leu trp gly	thr ser thr gln leu ser asn asp gly asn
1321/441	1351/451
GCA AAG GGC TTT TCA CCT GAG TCT CTC ATC	CAT GGA ATT GCT GAG TCT CAG TTA TGC TAC
ala lys gly phe ser pro glu ser leu ile	his gly ile ala glu ser gln leu cys tyr
1381/461	1411/471
ATA AAG CAG GGA ATC TTC TCA GTG ACG AAC	CCA CAT CCT GAA ATT TTC CTA GTT GTG AGA
ile lys gln gly ile phe ser val thr asn	pro his pro glu ile phe leu val val arg
1441/481	1471/491
ATT GAA AAG GTG CTG CAG GGA AAC ATC ACA	CAC TGT GCA GAA CCC TAC ATC AAA AAC TCA
ile glu lys val leu gln gly asn ile thr	his cys ala glu pro tyr ile lys asn ser
1501/501	1531/511
GAT CCG ATA AAG ACA GCC CAG AAG GTA CAC	AGG ACA GCT AAA CAA GTG TGT AGT CGC CTT
asp pro ile lys thr ala gln lys val his	arg thr ala lys gln val cys ser arg leu
1561/521	1591/531
GGA CAA TAC AGA ATG CCA TTT GCT TGG GCA	GCC AGA CCC ATT TTC AAA GAT GTT CAG GGC
gly gln tyr arg met pro phe ala trp ala	ala arg pro ile phe lys asp val gln gly
1621/541	1651/551
TCT CTG GAT CTG GAT GGG AGA TTT TCC CCT	TTG TAT AAA CAA GAC AGT AGC AAG CTT TCA
ser leu asp leu asp gly arg phe ser pro	leu tyr lys gln asp ser ser lys leu ser
1681/561	1711/571
AAT GAA GAT ATT CTC AAG TTG CTC TCA GAA	TAC AAA AAG CCA GAG AAG ACA AAA TTG CAG
asn glu asp ile leu lys leu leu ser glu	tyr lys lys pro glu lys thr lys leu gln
1741/581	1771/591
ATT ATC CCT GGA CAG CTG AGT ATC ACA GTG	GAA TGT GTT CCT GTA GAT TTA CCA AAT TGT
ile ile pro gly gln leu ser ile thr val	glu cys val pro val asp leu pro asn cys
1801/601	1831/611
ATT ACC TCT TCA TAT GTG CCC CTG AAG CCT	TTT GAA AAG AAT TGT CAG AAT ATT ACT GTG
ile thr ser ser tyr val pro leu lys pro	phe glu lys asn cys gln asn ile thr val
1861/621	1891/631
GAG GTT GAA GAG TTT GTT CCA GAA ATG ACA	AAA TAT TGT TAT CCA TTC ACT ATT TAC AAA
glu val glu glu phe val pro glu met thr	lys tyr cys tyr pro phe thr ile tyr lys
1921/641	1951/651
AAT CAT CTG TAT GTA TAT CCC TTG CAA TTA	AAA TAT GAC AGC CAG AAA TCG TTT GCC AAG
asn his leu tyr val tyr pro leu gln leu	lys tyr asp ser gln lys ser phe ala lys
1981/661	2011/671
GCT AGG AAC ATT GCT GTC TGT GTG GAA TTC	CGG GAT TCG GAT GAA AGT GAC GCG TCT GCG
ala arg asn ile ala val cys val glu phe	arg asp ser asp glu ser asp ala ser ala
2041/681	2071/691
CTA AAG TGC ATT TAC GGA AAA CCA GCA GGG	TCT GTT TTT ACC ACA AAT GCT TAT GCT GTG
leu lys cys ile tyr gly lys pro ala gly	ser val phe thr thr asn ala tyr ala val

Figure 1 (20 of 35)

21/95

2101/701	2131/711
GTC TCG CAT CAC AAC CAA AAT CCG GAG TTC	TAT GAT GAG ATC AAA ATT GAG CTT CCC ATT
val ser his his asn gln asn pro glu phe	tyr asp glu ile lys ile glu leu pro ile
2161/721	2191/731
CAC CTG CAC CAG AAG CAT CAC CTG CTT TTT	ACT TTT TAT CAT GTG AGT TGT GAA ATC AAC
his leu his gln lys his his leu leu phe	thr phe tyr his val ser cys glu ile asn
2221/741	2251/751
ACA AAA GGA ACA ACC AAA AAG CAA GAC ACA	GTG GAA ACT CCA GTG GGA TTT GCC TGG GTA
thr lys gly thr thr lys lys gln asp thr	val glu thr pro val gly phe ala trp val
2281/761	2311/771
CCT TTG CTG AAG GAT GGG AGG GTC ATC ACA	TTG GAG CAG CAG CTG CCA GTC TCA GCC AAT
pro leu leu lys asp gly arg val ile thr	leu glu gln gln leu pro val ser ala asn
2341/781	2371/791
CTT CCT CCA GGC TAC TTG AAT GTG AAT GAT	GCT GAA TCA AGA AGG CAA TCA AAT GCG GAT
leu pro pro gly tyr leu asn val asn asp	ala glu ser arg arg gln ser asn ala asp
2401/801	2431/811
ATC AAG TGG GTA GAT GGT GCA AAG CCT TTG	CTG AAG ATT AAG ACC CAC TTA GAA TCA ACC
ile lys trp val asp gly ala lys pro leu	leu lys ile lys thr his leu glu ser thr
2461/821	2491/831
ATT TAT ACT CAG GAT CTG CAT GTG CAC AAA	TTC TTC CAT CAT TGC CAG CTG ATT CAG TCG
ile tyr thr gln asp leu his val his lys	phe phe his his cys gln leu ile gln ser
2521/841	2551/851
GGC TCA AAA GAA GTT CCA GGG GAA CTC ATT	AAA TAT TTA AAG TGT TTG CAT GCC ATG GAG
gly ser lys glu val pro gly glu leu ile	lys tyr leu lys cys leu his ala met glu
2581/861	2611/871
ATC CAA GTC ATG ATA CAG TTT CTA CCT GTA	ATT CTT ATG CAA CTC TTC CGA GTT CTC ACA
ile gln val met ile gln phe leu pro val	ile leu met gln leu phe arg val leu thr
2641/881	2671/891
AAC ATG ACC CAT GAA GAT GAC GTT CCC ATC	AAC TGC ACC ATG GTT CTC TTA CAC ATT GTG
asn met thr his glu asp asp val pro ile	asn cys thr met val leu leu his ile val
2701/901	2731/911
TCT AAG TGT CAT GAA GAA GGC TTG GAG AGC	TAC TTA AGA TCC TTC ATA AAG TAT AGC TTC
ser lys cys his glu glu gly leu glu ser	tyr leu arg ser phe ile lys tyr ser phe
2761/921	2791/931
AGA CCT GAA AAA CCA AGC ACT CTT CAG GCC	CAG TTG ATA CAT GAA ACC CTG GCT ACG ACT
arg pro glu lys pro ser thr leu gln ala	gln leu ile his glu thr leu ala thr thr
2821/941	2851/951
ATG ATA GCA ATA TTG AAA CAG TCT GCA GAT	TTC CTA GCC ATA AAT AAA CTT CTA AAG TAC
met ile ala ile leu lys gln ser ala asp	phe leu ala ile asn lys leu leu lys tyr
2881/961	2911/971
TCA TGG TTT TTC TTT GAA ATA ATT GCA AAG	TCG ATG GCC ACA TAC TTA TTG GAA GAG AAT
ser trp phe phe phe glu ile ile ala lys	ser met ala thr tyr leu leu glu glu asn
2941/981	2971/991
AAA ATT AAG CTC CCC AGG GGC CAA AGG TTT	CCT GAG GCG TAT CAC CAC GTC TTA CAT TCT
lys ile lys leu pro arg gly gln arg phe	pro glu ala tyr his his val leu his ser
3001/1001	3031/1011
CTG CTC CTT GCA ATA ATT CCC CAT GTG ACC	ATT CGC TAT GCA GAG ATT CCT GAT GAG TCC
leu leu leu ala ile ile pro his val thr	ile arg tyr ala glu ile pro asp glu ser
3061/1021	3091/1031
CGA AAT GGG AAT TAT AGC TTA GCC AGC TTT	CTG AAG GCG TGC TTG ACA CTG ATG GAC AGA
arg asn gly asn tyr ser leu ala ser phe	leu lys arg cys leu thr leu met asp arg
3121/1041	3151/1051
GGA TTT GTT TTC AAT TTG ATA AAT GAC TAT	ATA TCA GGA TTT AGC CCT AAG GAT CCT AAG
gly phe val phe asn leu ile asn asp tyr	ile ser gly phe ser pro lys asp pro lys
3181/1061	3211/1071
GTT CTT GCT GAA TAC AAG TTT GAA TTT CTC	CAA ACA ATC TGC AAT CAT GAA CAT TAC ATT
val leu ala glu tyr lys phe glu phe leu	gln thr ile cys asn his glu his tyr ile

16

Figure X (21 of 35)

3241/1081	3271/1091
CCT CTG AAC TTG CCA ATG GCA TTT GCA AAG	CCT AAA TTA CAG AGA GTT CAA GAT TCC AAT
pro leu asn leu pro met ala phe ala lys	pro lys leu gln arg val gln asp ser asn
3301/1101	3331/1111
CTT GAA TAC AGT TTA TCA GAT GAG TAT TGC	AAG CAT CAC TTC TTG GTT GGC CTA CTT CTG
leu glu tyr ser leu ser asp glu tyr cys	lys his his phe leu val gly leu leu leu
3361/1121	3391/1131
CGG GAA ACC TCC ATT GCT CTT CAA GAC AAC	TAT GAG ATC AGA TAC ACA GCT ATC TCA GTC
arg glu thr ser ile ala leu gln asp asn	tyr glu ile arg tyr thr ala ile ser val
3421/1141	3451/1151
ATA AAG AAT CTT TTG ATA AAA CAT GCA TTT	GAT ACT AGA TAC CAG CAC AAG AAC CAG CAA
ile lys asn leu leu ile lys his ala phe	asp thr arg tyr gln his lys asn gln gln
3481/1161	3511/1171
GCC AAA ATA GCG CAG TTG TAC CTC CCA TTT	GTC GGA CTG CTC TTG GAA AAT ATC CAG CGA
ala lys ile ala gln leu tyr leu pro phe	val gly leu leu leu glu asn ile gln arg
3541/1181	3571/1191
CTG GCA GGC CGA GAT ACT CTG TAT TCC TGT	GCA GCC ATG CCT AGT TCT GCA TCT AGG GAT
leu ala gly arg asp thr leu tyr ser cys	ala ala met pro ser ser ala ser arg asp
3601/1201	3631/1211
GAG TTT CCA TGT GGC TTT GTT TCA CCT ACA	AAC AGA GGG AGC CTG GCC AGT GAC AAA GAC
glu phe pro cys gly phe val ser pro thr	asn arg gly ser leu ala ser asp lys asp
3661/1221	3691/1231
ACA GCC TAT GGG TCA TTT CAA AAT GGT CAT	GGA ATT AAG AGG GAA GAT TCA AGA GGT TCC
thr ala tyr gly ser phe gln asn gly his	gly ile lys arg glu asp ser arg gly ser
3721/1241	3751/1251
CTT ATT CCT GAA GGA GCA ACA GGA TTT CCA	GAC CCT GGG AGC ACT AGT GAA AAC ACA CGA
leu ile pro glu gly ala thr gly phe pro	asp pro gly ser thr ser glu asn thr arg
3781/1261	3811/1271
CAG AGT TCT TCA AGG AGT AGT GTA TCC CAG	TAT AAT CGT CTG GAT CAG TAT GAA ATC AGA
gln ser ser ser arg ser ser val ser gln	tyr asn arg leu asp gln tyr glu ile arg
3841/1281	3871/1291
AAC CTC TTG ATG TGC TAC TTA TAC ATA GTA	AAG ATG ATT TCT GAA GAT ACT CTC TTG ACT
asn leu leu met cys tyr leu tyr ile val	lys met ile ser glu asp thr leu leu thr
3901/1301	3931/1311
TAC TGG AAT AAA GTG TCT CCT CAG GAG CTC	ATA AAC ATT CTT GTA CTT CTA GAA GTA TGT
tyr trp asn lys val ser pro gln glu leu	ile asn ile leu val leu leu glu val cys
3961/1321	3991/1331
TTG TTT CAC TTC CGA TAT ATG GGG AAA AGA	AAC ATA GCA AGG GTA CAT GAT GCC TGG CTA
leu phe his phe arg tyr met gly lys arg	asn ile ala arg val his asp ala trp leu
4021/1341	4051/1351
TCC AAA CAC TTT GGA ATA GAT AGA AAA TCA	CAA ACT ATG CCA GCT CTT CGA AAC AGA TCA
ser lys his phe gly ile asp arg lys ser	gln thr met pro ala leu arg asn arg ser
4081/1361	4111/1371
GGG GTG ATG CAA GCT CGG CTT CAA CAT CTC	AGC AGC TTA GAA AGC TCA TTC ACA CTT AAT
gly val met gln ala arg leu gln his leu	ser ser leu glu ser ser phe thr leu asn
4141/1381	4171/1391
CAC AGT TCT GCA ACA ACG GAA GCA GAC ATT	TTC CAC CAG GCG CTT CTG GAA GGC AAT ACT
his ser ser ala thr thr glu ala asp ile	phe his gln ala leu leu glu gly asn thr
4201/1401	4231/1411
GCT ACT GAA GTA TCT CTG ACA GTA CTA GAG	ACG ATC TCC TTT TTT ACC CAG TGC TTC AAG
ala thr glu val ser leu thr val leu glu	thr ile ser phe phe thr gln cys phe lys
4261/1421	4291/1431
AAC CAA CTT TTA AAT AAT GAT GGT CAC AAC	CCA CTA ATG AAA AAA GTA TTT GAT ATT CAC
asn gln leu leu asn asn asp gly his asn	pro leu met lys lys val phe asp ile his
4321/1441	4351/1451
CTT GCT TTT CTT AAA AAT GGA CAA TCT GAA	GTG TCA CTG AAG CAT GTC TTT GCC TCA CTG
leu ala phe leu lys asn gly gln ser glu	val ser leu lys his val phe ala ser leu

23/95

4381/1461	4411/1471
AGA TCT TTC ATC AGT AAG TTT CCC TCA GCC	TTT TTC AAA GGA AGA GTA AAC ATG TGT GCT
arg ser phe ile ser lys phe pro ser ala	phe phe lys gly arg val asn met cys ala
4441/1481	4471/1491
GCA TTT TGC TAT GAG GTT TTA AAG TGC TGT	ACT TCA AAG ATT AGC TCA ACC AGG AAT GAG
ala phe cys tyr glu val leu lys cys cys	thr ser lys ile ser ser thr arg asn glu
4501/1501	4531/1511
GCA TCT GCA CTT TTG TAT CTT TTG ATG AGA	AAC AAC TTT GAA TAT ACC AAG AGG AAA ACC
ala ser ala leu leu tyr leu leu met arg	asn asn phe glu tyr thr lys arg lys thr
4561/1521	4591/1531
TTT CTG AGG ACA CAC TTG CAG ATA ATC ATT	GCT GTG AGT CAG CTA ATA GCT GAT GTA GCA
phe leu arg thr his leu gln ile ile ile	ala val ser gln leu ile ala asp val ala
4621/1541	4651/1551
CTA AGT GGA GGA TCG AGA TTT CAA GAG TCT	TTA TTC ATT ATC AAT AAC TTT GCA AAT AGC
leu ser gly gly ser arg phe gln glu ser	leu phe ile ile asn asn phe ala asn ser
4681/1561	4711/1571
GAC AGA CCT ATG AAG GCA ACT GCT TTT CCC	ACA GAA GTC AAA GAT TTG ACC AAG AGG ATC
asp arg pro met lys ala thr ala phe pro	thr glu val lys asp leu thr lys arg ile
4741/1581	4771/1591
CGC ACC GTT CTT ATG GCC ACT GCC CAA ATG	AAG GAA CAT GAG AAA GAC CCT GAA ATG CTA
arg thr val leu met ala thr ala gln met	lys glu his glu lys asp pro glu met leu
4801/1601	4831/1611
ATT GAT CTC CAG TAT AGC TTA GCT AAA TCT	TAT GCC AGC ACA CCA GAG CTG AGG AAA ACT
ile asp leu gln tyr ser leu ala lys ser	tyr ala ser thr pro glu leu arg lys thr
4861/1621	4891/1631
TGG CTT GAC AGC ATG GCC AAA ATT CAT ATA	AAA AAT GGA GAT TTT TCT GAG GCT GCA ATG
trp leu asp ser met ala lys ile his ile	lys asn gly asp phe ser glu ala ala met
4921/1641	4951/1651
TGT TAT GTC CAT GTA GCG GCT CTA GTT GCA	GAA TTT CTT CAC CGA AAG AAA TTA TTC CCT
cys tyr val his val ala ala leu val ala	glu phe leu his arg lys lys leu phe pro
4981/1661	5011/1671
AGT GGG TGT TCA GCG TTC AAG AAA ATT ACT	CCC AAT ATA GAT GAA GAA GGA GCC ATG AAA
ser gly cys ser ala phe lys lys ile thr	pro asn ile asp glu glu gly ala met lys
5041/1681	5071/1691
GAA GAT GCC GGG ATG ATG GAT GTT CAT TAC	AGT GAA GAG GTT TTG CTG GAA TTG CTA GAA
glu asp ala gly met met asp val his tyr	ser glu glu val leu leu glu leu leu glu
5101/1701	5131/1711
CAG TGT GTG GAT GGT TTG TGG AAG GCA GAG	CGA TAT GAA GTA ATT TCT GAG ATT TCC AAG
gln cys val asp gly leu trp lys ala glu	arg tyr glu val ile ser glu ile ser lys
5161/1721	5191/1731
TTG ATT ATT CCA ATT TAT GAG AAA CGC CGT	GAA TTT GAG AAA CTG ACT CAA GTT TAT AGA
leu ile ile pro ile tyr glu lys arg arg	glu phe glu lys leu thr gln val tyr arg
5221/1741	5251/1751
ACT CTC CAT GGC GCT TAC ACA AAA ATT TTG	GAG GTT ATG CAC ACC AAA AAA CGA CTT TTA
thr leu his gly ala tyr thr lys ile leu	glu val met his thr lys lys arg leu leu
5281/1761	5311/1771
GGT ACT TTC TTT AGA GTT GCC TTT TAT GGC	CAG TCT TTT TTT GAA GAA GAA GAT GGA AAG
gly thr phe phe arg val ala phe tyr gly	gln ser phe phe glu glu glu asp gly lys
5341/1781	5371/1791
GAG TAT ATC TAT AAG GAA CCC AAG CTC ACT	GGC CTT TCA GAG ATT TCC TTG AGA CTT GTG
glu tyr ile tyr lys glu pro lys leu thr	gly leu ser glu ile ser leu arg leu val
5401/1801	5431/1811
AAA CTT TAC GGG GAG AAA TTT GGT ACT GAA	AAT GTC AAA ATA ATT CAG GAT TCA GAC AAG
lys leu tyr gly glu lys phe gly thr glu	asn val lys ile ile gln asp ser asp lys
5461/1821	5491/1831
GTA AAT GCC AAA GAG CTT GAT CCA AAA TTC	GCT CAT ATA CAA GTC ACT TAT GTG AAG CCG
val asn ala lys glu leu asp pro lys phe	ala his ile gln val thr tyr val lys pro

24/95

5521/1841	5551/1851
TAT TTT GAT GAC AAA GAA CTC ACA GAA AGA	AAG ACG GAG TTT GAA AGA AAT CAT AAT ATC
tyr phe asp asp lys glu leu thr glu arg	lys thr glu phe glu arg asn his asn ile
5581/1861	5611/1871
AAC AGA TTT GTT TTT GAG GCC CCA TAT ACA	TTA TCA GGC AAG AAA CAA GGT TGC ATT GAA
asn arg phe val phe glu ala pro tyr thr	leu ser gly lys lys gln gly cys ile glu
5641/1881	5671/1891
GAA CAG TGC AAG CGT CGT ACT ATC TTG ACC	ACT TCA AAC TCA TTT CCA TAT GTA AAA AAG
glu gln cys lys arg arg thr ile leu thr	thr ser asn ser phe pro tyr val lys lys
5701/1901	5731/1911
AGG ATA CCT ATA AAC TGT GAA CAG CAG GTG	AAT TTA AAA CCA ATT GAT GTT GCT ACT GAT
arg ile pro ile asn cys glu gln gln val	asn leu lys pro ile asp val ala thr asp
5761/1921	5791/1931
GAA ATC AAA GAT AAA ACT GCA GAG CTA CAC	AAG CTC TGC TCC TCT GTT GAC GTG GAC ATG
glu ile lys asp lys thr ala glu leu his	lys leu cys ser ser val asp val asp met
5821/1941	5851/1951
ATT CAG CTT CAG CTA AAG TTG CAG GGC TGT	GTC TCT GTG CAG GTC AAT GCT GGT CCA TTA
ile gln leu gln leu lys leu gln gly cys	val ser val gln val asn ala gly pro leu
5881/1961	5911/1971
GCA TAT GCG AGG GCT TTC TTA AAT GAA AGT	CAA GCT AAC AAG TAT CCA CCT AAA AAA GTG
ala tyr ala arg ala phe leu asn glu ser	gln ala asn lys tyr pro pro lys lys val
5941/1981	5971/1991
AAT GAG TTG AAG GAC ATG TTT AGA AAA TTC	ATA CAA GCA TGC AGC ATT GCA CTT GAA CTA
asn glu leu lys asp met phe arg lys phe	ile gln ala cys ser ile ala leu glu leu
6001/2001	6031/2011
AAT GAG CGG CTA ATT AAA GAG GAT CAA ATT	GAG TAC CAT GAA GGG CTA AAG TCA AAT TTC
asn glu arg leu ile lys glu asp gln ile	glu tyr his glu gly leu lys ser asn phe
6061/2021	6091/2031
AGA GAC ATG GTA AAA GAA CTG TCT GAC ATT	ATC CAT GAG CAG ATA CTA CAA GAA GAC ACA
arg asp met val lys glu leu ser asp ile	ile his glu gln ile leu gln glu asp thr
6121/2041	6151/2051
ATG CAT TCT CCC TGG ATG AAC AAC ACA TTA	CAT GTA TTT TGT GCA ATT AGT GGT ACA TCA
met his ser pro trp met asn asn thr leu	his val phe cys ala ile ser gly thr ser
6181/2061	6211/2071
AGT AAC AGA GGT TAT GGT TCC CCA AGA TAC	GCG GAA GTA TGA AGA GAT TTG GAA GGA AAT
ser asn arg gly tyr gly ser pro arg tyr	ala glu val OPA
6241/2081	6271/2091
GGC AAT GAG ACT GAC CTT TCT CAG GAA TAT	TTG GAG CTG TGC AAC TGT TAG CAT TTA GAG
6301/2101	6331/2111
ATT TGA TAT GTG TGG AGT GTT GCC TCC TGA	CAC CAA AAT CGT CAT GCT TTC ATA CAG GGT
6361/2121	6391/2131
GCT TGT ATC TGT AAA TAT TTA AGC AAC TCG	AAG TGC CTG AAA AAT TGC AGC ACT GTG CTT
6421/2141	6451/2151
GCT TGT ACT TTT TTT AGG TAA ATC TAT ATG	CTG AAA AGT AGA GCT CAA AAC CAT TCG TTC
6481/2161	6511/2171
AAT TGC TTA GTT ACC ACT TAC TAA TAA TGA	GAA TAT GTA AAA TGT ATA AAT GGA AAC CCA
6541/2181	6571/2191
AAT AAA AGG TAA CAA ACT TAT TTG TAA AAA	AAA AAA AAA

E. Mouse CLASP-5 cDNA sequence

-282/1 -252/11
 GGA CAC TGA CAT GGA CTG AAG GAG TAG AAA ACT TCC TCA TAC AAG CAC AAG CCA CAG CCA
 -222/21 -192/31
 CTC TCT CTG GCT GAT CTA GTG GTT ATC TTG AGA AGG TTA GGT TCT TTT TTG TTT CTA CTT
 -162/41 -132/51
 ATT ACT TCA AAG CCA CTT CTG CTC TTC GAA ATT TTG TAA CCT TCC CCT GTT TCC TGT AGC
 -102/61 -72/71
 CGC CAT TTT GTC GCC CGT GAC AGT TTA CCC ACC GCG TTA ACT GTG TGT CTT CAG CCT CAG
 -42/81 -12/91
 CTT TAT GAG CCT GTC GAG CCA GTG GAC TTT GAA GGA CTC GTG ATG ACA CAC TTA AAC AGC
 met thr his leu asn ser
 19/101 49/111
 TTG GAT GCA GAG CTG GCC CAG GAG CTG GGG GAC CTC ACC GAT GAC GAC CTG CAT GTG GCC
 leu asp ala glu leu ala gln glu leu gly asp leu thr asp asp asp leu his val ala
 79/121 109/131
 TTC ACA CCC AAA GAA TGT AGG ACT TTG CAG CAC TCT CTG CCA GAG GAA GGA GTT GAA CTG
 phe thr pro lys glu cys arg thr leu gln his ser leu pro glu glu gly val glu leu
 139/141 169/151
 GAT CCT CAC GTC AGA GAC TGT GTT CAG ACC TAT ATT CGA GAG TGG CTG ATT GTA AAC CGG
 asp pro his val arg asp cys val gln thr tyr ile arg glu trp leu ile val asn arg
 199/161 229/171
 AAA AAC CAA GGA AGT TCA GAG TTT TGC AGC TTT AAA AAG ACG GGA TCT CGC AGA GAT TTT
 lys asn gln gly ser ser glu phe cys ser phe lys lys thr gly ser arg arg asp phe
 259/181 289/191
 CAG AAG ACG CTT CAG AAA CAG ACG TTT GAG TCA GAA ACC TTG GAG TGC AGT GAA CCG GAC
 gln lys thr leu gln lys gln thr phe glu ser glu thr leu glu cys ser glu pro asp
 319/201 349/211
 ACT CAG ACA GGA CCC CGT CAT CCC TTA AAC GTG CTG TGT GAC GTG TCT GGG AAG GGC CCC
 thr gln thr gly pro arg his pro leu asn val leu cys asp val ser gly lys gly pro
 379/221 409/231
 CTC ACT TCT TGT GAC TTC GAC CTC CGC AGC CTG CAG CCT GAT GAG CGG CTG GAA AAC CTG
 leu thr ser cys asp phe asp leu arg ser leu gln pro asp glu arg leu glu asn leu
 439/241 469/251
 CTC CAG CTT GTG AGC GCT GAG GAC TTT GAG AAG GAG AAG GAG GAG GCC CGC AAG ACC AAT
 leu gln leu val ser ala glu asp phe glu lys glu lys glu glu ala arg lys thr asn
 499/261 529/271
 CGG CCG GCT GAG CTC TTT GCC CTC TAT CCG CCC GTG GAT GAG GAG GAT GCT GTG GAA ATA
 arg pro ala glu leu phe ala leu tyr pro pro val asp glu glu asp ala val glu ile
 559/281 589/291
 CGT CCA GTA CCT GAA TGT CCT AAG GAA CAT CTG GGC AAC AGA ATA TTG GTC AAG GTG CTG
 arg pro val pro glu cys pro lys glu his leu gly asn arg ile leu val lys val leu
 619/301 649/311
 ACT CTG AAG TTT GAG ATT GAA ATT GAA CCT CTG TTT GCC AGT ATT GCC CTC TAT GAC GTT
 thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile ala leu tyr asp val
 679/321 709/331
 AAA GAA AGG AAA AAG ATC TCA GAA AAT TTC CAC TGT GAC CTG AAC TCC GAC CAG TTC AAA
 lys glu arg lys lys ile ser glu asn phe his cys asp leu asn ser asp gln phe lys
 739/341 769/351
 GGG TTT CTG CGA GCT CAC ACA CCC TCG ATT GAC CCA TCG AGT CAG GCT AGG TCT GCC GTG
 gly phe leu arg ala his thr pro ser ile asp pro ser ser gln ala arg ser ala val

26/95

799/361	829/371
TTC TCC GTC ACC TAC CCA TCT TCA GAC ATC	TAC CTG GTT GTC AAG ATT GAA AAG GTC CTT
phe ser val thr tyr pro ser ser asp ile	tyr leu val val lys ile glu lys val leu
859/381	889/391
CAG CAA GGA GAG ATT GCA GAC TGT GCA GAA	CCC TAC ATG ATC ATC AAA GAA AGC GAT GGT
gln gln gly glu ile ala asp cys ala glu	pro tyr met ile ile lys glu ser asp gly
919/401	949/411
GGA AAG AGT AAA GAA AAG GTT GAA AAA CTA	AAA CTT CAA GCT GAA TCC TTC TGC CAA CGT
gly lys ser lys glu lys val glu lys leu	lys leu gln ala glu ser phe cys gln arg
979/421	1009/431
TTG GGG AAA TAC CGG ATG CCC TTC GCC TGG	GCC CCC ATT AGC TTA GCA AGC TTC TTC AAC
leu gly lys tyr arg met pro phe ala trp	ala pro ile ser leu ala ser phe phe asn
1039/441	1069/451
GTC TCC ACC CTT GAA AGG GAG AGC ACA GAT	GTG GAG CCT GGG GTT GGG AGG AAC TCT GTG
val ser thr leu glu arg glu ser thr asp	val glu pro gly val gly arg asn ser val
1099/461	1129/471
GGT GAG AAG AGG AGC TTG TCC CAA TCC AGG	AGG CCC TCT GAG CGA ACC CTC TCC TTG GAG
gly glu lys arg ser leu ser gln ser arg	arg pro ser glu arg thr leu ser leu glu
1159/481	1189/491
GAA AAT GGA GTT GGA TCC AAC TTC AAA GCC	ACC ACC TTG GCC ACC AAC ATC TTC TTC AAA
glu asn gly val gly ser asn phe lys ala	thr thr leu ala thr asn ile phe phe lys
1219/501	1249/511
CAG GAG GGA GAT CGC CTT AGT GAT GAA GAC	TTG TTC AAG TTT TTA GCT GAC TAC AAG AGA
gln glu gly asp arg leu ser asp glu asp	leu phe lys phe leu ala asp tyr lys arg
1279/521	1309/531
TCT TCA TCC CTA CAG CGA AGA GTC AAA TCC	ATC CCA GGC TCA CTG AGG CTG GAG ATA TCC
ser ser ser leu gln arg arg val lys ser	ile pro gly ser leu arg leu glu ile ser
1339/541	1369/551
CCA GCT CCC GAC GTG ATG AAC TGC TGC CTG	ACG CCC GAG ATG CTG CCA GTC AAA CCT TTT
pro ala pro asp val met asn cys cys leu	thr pro glu met leu pro val lys pro phe
1399/561	1429/571
CCT GAA AAT CGG ACG CGT CCA CAC AAG GAG	ATT TTG GAA TTT CCG ATC CGG GAG GTG TAC
pro glu asn arg thr arg pro his lys glu	ile leu glu phe pro ile arg glu val tyr
1459/581	1489/591
GTC CCT CAC ACT GTG TAC AGA AAC CTT CTG	TAC GTA TAC CCC CAG CGA CTG AAC TTC GCT
val pro his thr val tyr arg asn leu leu	tyr val tyr pro gln arg leu asn phe ala
1519/601	1549/611
AGC AAG CTA GCA TCT GCC CGG AAC ATC ACA	ATA AAG ATT CAG TTT ATG TGC GGA GAA GAC
ser lys leu ala ser ala arg asn ile thr	ile lys ile gln phe met cys gly glu asp
1579/621	1609/631
CCC AGC AAT GCT ATG CCG GTC ATC TTT GGC	AAG TCC AGT GGG CCT GAA TTT CTG CAG GAA
pro ser asn ala met pro val ile phe gly	lys ser ser gly pro glu phe leu gln glu
1639/641	1669/651
GTA TAT ACA GCT ATT ACA TAC CAT AAT AAG	TCT CCT GAC TTT TAC GAA GAA GTG AAA ATT
val tyr thr ala ile thr tyr his asn lys	ser pro asp phe tyr glu glu val lys ile
1699/661	1729/671
AAG CTC CCT GCC AAG CTC ACA GTG AAT CAT	CAC CTC CTC TTC ACC TTC TAC CAC ATC AGC
lys leu pro ala lys leu thr val asn his	his leu leu phe thr phe tyr his ile ser
1759/681	1789/691
TGT CAG CAG AAG CAA GGG GCC TCC GGA GAA	AGC CTT CTG GGG TAC TCG TGG CTG CCG ATT
cys gln gln lys gln gly ala ser gly glu	ser leu leu gly tyr ser trp leu pro ile
1819/701	1849/711
CTG TTA AAC GAA CGT CTT CAA ACC GGA TCC	TAC TGT CTG CCT GTT GCC TTG GAA AAA CTA
leu leu asn glu arg leu gln thr gly ser	tyr cys leu pro val ala leu glu lys leu
1879/721	1909/731
CCA CCC AAC TAC TCC ATA CAT TCT GCT GAG	AAA GTC CCT TTA CAG AAT CCT CCC ATT AAG
pro pro asn tyr ser ile his ser ala glu	lys val pro leu gln asn pro pro ile lys

Figure ¹⁶ (26 of 35)

27/95

1939/741	1969/751
TGG GTC GAG GGC CAT AAG GGA GTA TTT AAT	ATT GAA GTG CAA GCT GTT TCT TCC GTC CAC
trp val glu gly his lys gly val phe asn	ile glu val gln ala val ser ser val his
1999/761	2029/771
ACC CAG GAT AAC CAC CTG GAG AAG TTC TTC	ACC CTT TGC CAC TCC CTG GAG AGC CAG GTG
thr gln asp asn his leu glu lys phe phe	thr leu cys his ser leu glu ser gln val
2059/781	2089/791
AGC TTC CCT ATC CGT GTG CTG GAC CAG AAG	ATC ACC GAG AGC ACG CTG GAG CAC GAG CTG
ser phe pro ile arg val leu asp gln lys	ile thr glu ser thr leu glu his glu leu
2119/801	2149/811
AAA CTC AGC ATC ATC TGC CTC AAC TCC TCC	CGC CTG GAG CCC CTC GTG CTC TTC CTC CAC
lys leu ser ile ile cys leu asn ser ser	arg leu glu pro leu val leu phe leu his
2179/821	2209/831
CTG GTG CTC GAC AAG CTG TTC CAG CTT TCC	GTG CAG CCC ATG GTC ATT GCT GGC CAA ACA
leu val leu asp lys leu phe gln leu ser	val gln pro met val ile ala gly gln thr
2239/841	2269/851
GCA AAC TTC TCC CAG TTT GCC TTC GAG TCT	GTG GTG GCC ATT GCC AAT AGC CTG CAC AAC
ala asn phe ser gln phe ala phe glu ser	val val ala ile ala asn ser leu his asn
2299/861	2329/871
AGC AAG GAC CTG AGG AAG GAC CAG CAC GGA	AGG AAC TGC CTT CTG GCC TCC TAT GTG CAC
ser lys asp leu arg lys asp gln his gly	arg asn cys leu leu ala ser tyr val his
2359/881	2389/891
TAC GTG TTC CGG CTG CCG GAA CTG CAC AGG	GAT ACA TCC AAG TCA GGT GGC CCC ATC ACC
tyr val phe arg leu pro glu leu his arg	asp thr ser lys ser gly gly pro ile thr
2419/901	2449/911
GTA GTC CCC GAC CCC CGA TAC CAC ACA TAT	GGA CGC ACA TCT GCC GCT GCA GTG AGT TCA
val val pro asp pro arg tyr his thr tyr	gly arg thr ser ala ala val ser ser
2479/921	2509/931
AAG CTG ATG CAG GCC CGT GTG ATG AGC AGC	AGC AAC CCA GAC CTG ACT GGG TCA CAC TGT
lys leu met gln ala arg val met ser ser	ser asn pro asp leu thr gly ser his cys
2539/941	2569/951
GCA GCC GAT GAG GAA GTT AAG AAC ATC ATG	TCT TCA AAG ATT GCC GAT CGC AAC TGC AGC
ala ala asp glu glu val lys asn ile met	ser ser lys ile ala asp arg asn cys ser
2599/961	2629/971
CGG ATG TCT TAC TAT TGC TCT GGC AAT AGT	GAT GCG CCA GGT TCA ACT GCA GCC CCA AGA
arg met ser tyr tyr cys ser gly asn ser	asp ala pro gly ser thr ala ala pro arg
2659/981	2689/991
CCA GTC AGC AAA AAG CAT TTC CAT GAG GAG	CTT GCC CTG CAG ATG GTG GTC AGC ACT GGA
pro val ser lys lys his phe his glu glu	leu ala leu gln met val val ser thr gly
2719/1001	2749/1011
GTA GTG AGA GAA ACG GTC TTC AAG TAC GCC	TGG TTC TTC TTT GAG CTT CTG GTG AAA AGC
val val arg glu thr val phe lys tyr ala	trp phe phe phe glu leu leu val lys ser
2779/1021	2809/1031
ATG GCG CAG TAT GTC CAT AAC CTG GAT AAA	CGG GAC AGT TTT CGG AGG ACT CGT TTT TCT
met ala gln tyr val his asn leu asp lys	arg asp ser phe arg arg thr arg phe ser
2839/1041	2869/1051
GAC CGC TTC AAA GAT GAC ATA ACT ACC ATT	GTT AAT GTG GTC ACC TCG GAG ATA GCA GCC
asp-arg phe lys asp asp ile thr thr ile	val asn val val thr ser glu ile ala ala
2899/1061	2929/1071
CTT TTA GTG AAA CCT CAG AAG GAA AGC GAG	CAG GCA GAA AAG ATC AAC ATC AGC CTT GCC
leu leu val lys pro gln lys glu ser glu	gln ala glu lys ile asn ile ser leu ala
2959/1081	2989/1091
TTC TTC CTG TAT GAC CTC CTG TCA ATC ATG	GAC AGA GGC TTC GTG TTC AAC CTC ATC AAG
phe phe leu tyr asp leu leu ser ile met	asp arg gly phe val phe asn leu ile lys
3019/1101	3049/1111
CAT TAC TGC AGC CAG CTG TCA GCC AAG CTG	AAT ATC CTT CCA ACG CTC ATC TCC ATG CGG
his tyr cys ser gln leu ser ala lys leu asn	ile leu pro thr leu ile ser met arg

3079/1121	3109/1131
CTG GAA TTC CTG AGG ATC CTC TGC AGC CAT	GAG CAC TAC CTC AAC TTG AAC CTC CTC TTC
leu glu phe leu arg ile leu cys ser his	glu his tyr leu asn leu asn leu leu phe
3139/1141	3169/1151
ATG AAT ACC GAC ACC GCA CCA GCA TCT CCC	TGC CCC TCC ATA TCC TCC CAG AAC TCG AGT
met asn thr asp thr ala pro ala ser pro	cys pro ser ile ser ser gln asn ser ser
3199/1161	3229/1171
TCC TGC TCC AGT TTC CAG GAC CAA AAG ATT	GCC AGC ATG TTC GAT CTG ACC CCG GAG TAC
ser cys ser ser phe gln asp gln lys ile	ala ser met phe asp leu thr pro glu tyr
3259/1181	3289/1191
CGG CAG CAG CAC TTC CTT ACA GGG CTG CTC	TTC ACG GAG CTG GCT GTT GCC CTG GAT GCT
arg gln gln his phe leu thr gly leu leu	phe thr glu leu ala val ala leu asp ala
3319/1201	3349/1211
GAG GGG GAT GGA ATT AGC AGA GTA CAG AGA	AAA GCC GTG AGT GCC ATC CAC AGC CTT CTG
glu gly asp gly ile ser arg val gln arg	lys ala val ser ala ile his ser leu leu
3379/1221	3409/1231
TGT TCT CAC GAC CTG GAT CCA CGG TGT CGC	AAA CCG GAA GTG AAA GTC AAA ATC GCC GCC
cys ser his asp leu asp pro arg cys arg	lys pro glu val lys val lys ile ala ala
3439/1241	3469/1251
CTT TAC CTG CCG TTG GTC GGC ATC ATT CTG	GAC GCT CTG CCA CAG CTC TAT GAC TTT ACA
leu tyr leu pro leu val gly ile ile leu	asp ala leu pro gln leu tyr asp phe thr
3499/1261	3529/1271
GAT GCT CGC AGT GGA AGG AGT CGT GCC AGT	GGC TCG TAT GAA GAA CAA GAT GTG GCC AAC
asp ala arg ser gly arg ser arg ala ser	gly ser tyr glu glu gln asp val ala asn
3559/1281	3589/1291
GGA ATC AAC CAG AAT GTG GCC CTG GCC ATA	GCG GGG AAT CAC TTT AAT TTG AAG ACC AGT
gly ile asn gln asn val ala leu ala ile	ala gly asn his phe asn leu lys thr ser
3619/1301	3649/1311
GGA GCA ATG CTG TCT TCC TTG CCC TAT AAG	CAG TAC AAC ATG CTG AAT GCA GAC ACC ACC
gly ala met leu ser ser leu pro tyr lys	gln tyr asn met leu asn ala asp thr thr
3679/1321	3709/1331
CGC CAC CTC ATG ATT TGC TTC CTG TGG ATC	ATG AAA AAT GCT GAT CAG AGC CTC ATC AGG
arg his leu met ile cys phe leu trp ile	met lys asn ala asp gln ser leu ile arg
3739/1341	3769/1351
AAG TGG ATC GCT GAC CTG CCT TCC ATG CAG	CTC AAT AGG ATT CTG GAC CTG CTG TTC ATC
lys trp ile ala asp leu pro ser met gln	leu asn arg ile leu asp leu leu phe ile
3799/1361	3829/1371
TGT GTC TCC TGC TTT GAA TAC AAG GGA AAG	CAG AGT TCT GAC AAA GTC AGT AAC CAG GTC
cys val ser cys phe glu tyr lys gly lys	gln ser ser asp lys val ser asn gln val
3859/1381	3889/1391
CTG CAG AAG TCA AGA GAC GTC AAG GCC AAG	CTG GAA GAG GCC CTG CTC CGT GGG GAA GGA
leu gln lys ser arg asp val lys ala lys	leu glu glu ala leu leu arg gly glu gly
3919/1401	3949/1411
GCC CGT GGG GAG ATG ATG CGC CGT CGC ATT	CCA GGG ACT GAC CGG TTT CCA GGC ATA AAT
ala arg gly glu met met arg arg arg-ile	pro gly thr asp arg phe pro gly ile asn
3979/1421	4009/1431
GAA AAT CTG AGA TGG AGG AAA GAG CAG ACA	CAG TGG CGG CAG GCT AAT GAG AAG CTG GAC
glu asn leu arg trp arg lys glu gln thr	gln trp arg gln ala asn glu lys leu asp
4039/1441	4069/1451
AAA ACA AAG GCA GAG TTA GAT CAA GAA GCC	TTG ATC AGT GGC AAC CTG GCT ACA GAA GCT
lys thr lys ala glu leu asp gln glu ala	leu ile ser gly asn leu ala thr glu ala
4099/1461	4129/1471
AAT TTG ATC ATC CTG GAT ATG CAG GAG AAC	ATC ATC CAG GCA AGC TCC GCC CTG GAC TGT
asn leu ile ile leu asp met gln glu asn	ile ile gln ala ser ser ala leu asp cys
4159/1481	4189/1491
AAA GAC AGC CTG CTG GGA GGT GTC CTC CGG	GTC CTG GTG AAT TCT CTG AGC TGT GAC CAG
lys asp ser leu leu gly gly val leu arg	val leu val asn ser leu ser cys asp gln

29/95

4219/1501	4249/1511
AGC ACC ACC TAC CTG ACT CAC TGT TTC GCA	ACC CTC CGA GCC CTC ATC GCC AAG TTT GGA
ser thr thr tyr leu thr his cys phe ala	thr leu arg ala leu ile ala lys phe gly
4279/1521	4309/1531
GAC CTG CTG TTC GAG GAG GAG ATG GAG CAG	TGT GCT GAC CTG TGT CAG CGG GTG CTA CAT
asp leu leu phe glu glu glu met glu gln	cys ala asp leu cys gln arg val leu his
4339/1541	4369/1551
CAC TGC AGC AGC AGC ATG GAC GTC ACA CGG	AGC CAA GCC TGC GCC ACC CTC TAC CTC CTC
his cys ser ser ser met asp val thr arg	ser gln ala cys ala thr leu tyr leu leu
4399/1561	4429/1571
ATG CGG TTC AGC TTC GGA GCC ACC AGT AAC	TTT GCA AGG GTA AAG ATG CAA GTG ACC ATG
met arg phe ser phe gly ala thr ser asn	phe ala arg val lys met gln val thr met
4459/1581	4489/1591
GCA CTG GCA TCC CTG GTA GGC AAA GCA CCA	GAC TTC AAC GAA GAG CAC CTG AGA AGG TCC
ala leu ala ser leu val gly lys ala pro	asp phe asn glu glu his leu arg arg ser
4519/1601	4549/1611
TTA AGG ACA ATT TTG GCC TAT TCA GAA GAG	GAC ACG GCC ATG CAG ACA ACT CCT TTT CCC
leu arg thr ile leu ala tyr ser glu glu	asp thr ala met gln thr thr pro phe pro
4579/1621	4609/1631
ATG CAG GTG GAG GAA CTT CTC TGC AAT CTG	AAC AGC ATT CTG TAC GAC ACA GTG AAG ATG
met gln val glu glu leu leu cys asn leu	asn ser ile leu tyr asp thr val lys met
4639/1641	4669/1651
AGG GAA TTC CAG GAA GAC CCT GAG ATG CTT	ATG GAC CTC ATG TAC AGA ATT GCC AAG AGC
arg glu phe gln glu asp pro glu met leu	met asp leu met tyr arg ile ala lys ser
4699/1661	4729/1671
TAC CAG GCA TCG CCT GAC CTG CGG CTG ACT	TGG CTC CAG AAC ATG GCA GAG AAA CAC ACT
tyr gln ala ser pro asp leu arg leu thr	trp leu gln asn met ala glu lys his thr
4759/1681	4789/1691
AAG AAG AAG TGC TTC ACA GAG GCC GCC ATG	TGC CTG GTG CAT GCA GCC GCC CTG GTG GCC
lys lys lys cys phe thr glu ala ala met	cys leu val his ala ala leu val ala
4819/1701	4849/1711
GAG TAC CTG AGC ATG CTG GAG GAC CAC AGC	TAC CTG CCG GTG GGC AGC GTC AGC TTT CAG
glu tyr leu ser met leu glu asp his ser	tyr leu pro val gly ser val ser phe gln
4879/1721	4909/1731
AAT ATT TCT TCC AAT GTG CTT GAG GAG TCT	GCA GTC TCT GAT GAC ACC TTG TCA CCT GAT
asn ile ser ser asn val leu glu glu ser	ala val ser asp asp thr leu ser pro asp
4939/1741	4969/1751
GAG GAC GGC GTA TGC TCT GGT CGG TAC TTC	ACT GAG AGT GGC CTG GTG GGC CTC CTG GAG
glu asp gly val cys ser gly arg tyr phe	thr glu ser gly leu val gly leu leu glu
4999/1761	5029/1771
CAG GCT GCG GAG CTC TTC AGC ACG GGA GGC	TTG TAC GAG ACG GTT AAT GAA GTC TAC AAG
gln ala ala glu leu phe ser thr gly gly	leu tyr glu thr val asn glu val tyr lys
5059/1781	5089/1791
CTG GTC ATC CCT ATC CTG GAG GCA CAC AGA	GAT TTC CGG AAG CTG ACC TCC ACT CAC GAC
leu val ile pro ile leu glu ala his arg	asp phe arg lys leu thr ser thr his asp
5119/1801	5149/1811
AAG CTG CAG AAG GCC TTC GAT AAC ATC ATC	AAC AAG GAC CAT AAG AGG ATG TTT GGG ACC
lys leu gln lys ala phe asp asn ile ile	asn lys asp his lys arg met phe gly thr
5179/1821	5209/1831
TAC TTC CGA GTT GGT TTC TAC GGA TCC CGA	TTT GGG GAT TTG GAT GAG CAG GAG TTC GTG
tyr phe arg val gly phe tyr gly ser arg	phe gly asp leu asp glu gln glu phe val
5239/1841	5269/1851
TAC AAG GAA CCC GCA ATC ACG AAG CTC CCG	GAG ATC TCA CAT AGA CTA GAG GGA TTT TAT
tyr lys glu pro ala ile thr lys leu pro	glu ile ser his arg leu glu gly phe tyr
5299/1861	5329/1871
GGC CAG TGT TTC GGT GCA GAG TTT GTG GAA	GTG ATA AAA GAC TCT ACT CCA GTG GAC AAA
gly gln cys phe gly ala glu phe val glu	val ile lys asp ser thr pro val asp lys

16

Figure 1 (29 of 35)

30/95

```

5359/1881
ACC AAG TTG GAT CCT AAC AAG GCC TAC ATT CAG ATC ACT TTT GTG GAG CCT TAC TTT GAT
thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro tyr phe asp
5419/1901
GAA TAT GAG ATG AAA GAC CGG GTG ACC TAC TTC GAG AAG AAT TTC AAC CTC CGG AGG TTC
glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu arg arg phe
5479/1921
ATG TAC ACC ACC CCC TTC ACC CTG GAG GGG AGA CCC CGG GGC GAG CTT CAT GAG CAA CAC
met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his glu gln his
5539/1941
CGC AGA AAC ACC GTG CTC ACC ACC ATG CAC GCC TTC CCC TAC ATC AAG ACC AGG ATC CGA
arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr arg ile arg
5599/1961
GTC AGC CAG AAA GAG GAG TTC GTT TTG ACT CCG ATT GAG GTT GCC ATT GAA GAT ATG AAG
val ser gln lys glu glu phe val leu thr pro ile glu val ala ile glu asp met lys
5659/1981
AAG AAG ACC CTG CAG TTA GCC GTG GCC ACT CAC CAG GAG CCC CCT GAT GCA AAG ATG CTG
lys lys thr leu gln leu ala val ala thr his gln glu pro pro asp ala lys met leu
5719/2001
CAA ATG GTA CTG CAG GGC TCT GTA GGA GCC ACT GTA AAT CAG GGA CCA CTG GAG GTG GCC
gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu glu val ala
5779/2021
CAA GTG TTC TTG GCT GAA ATT CCA GCT GAC CCA AAG CTC TAC CGA CAT CAC AAC AAG CTG
gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his asn lys leu
5839/2041
AGG TTG TGC TTC AAG GAG TTC ATA ATG CGA TGC GGA GAG GCC GTG GAG AAG AAC AGG CGA
arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys asn arg arg
5899/2061
CTC ATC ACC GCA GAG CAG CGG GAG TAC CAG CAG GAG CTG AAG AAG AAC TAC AAC AAG CTG
leu ile thr ala glu gln arg glu tyr gln gln glu leu lys lys asn tyr asn lys leu
5959/2081
AGA GAC AGC CTC AGG CCC ATG ATT GAG CGG AAA ATC CCA GAG CTC TAC AAG CCC ATA TTC
arg asp ser leu arg pro met ile glu arg lys ile pro glu leu tyr lys pro ile phe
6019/2101
AGA GTT GAC AGT CAG AAG AGG GAC TCT TTC CAC AGA TCT AGT TTC AGG AAA TGT GAA ACC
arg val asp ser gln lys arg asp ser phe his arg ser ser phe arg lys cys glu thr
6079/2121
CAG TTG TCA CAG GGC AGC TGA AAA AAG CCA CCT TTG CCG GTG ACG ACT GGG GCC CCA CTA
gln leu ser gln gly ser OPA
6139/2141
CTG GGA AGG ACT CGC TGG

```

F. mouse CLASP-7 cDNA Sequence

1. Fragment 1

```

1/1
CGC CGT CGG GGG CCC CAG GAT CGA GGC TAT AGT GGG GAT GAT GCC TGC AGC TTC TCT AGC
arg arg arg gly pro gln asp arg gly tyr ser gly asp asp ala cys ser phe ser ser
61/21
TTC CGC CCG GCC ACG TTA ACT GTC ACC AAC TTT TTC AAA CAG GAG GCA GAA CGG CTC AGT
phe arg pro ala thr leu thr val thr asn phe phe lys gln glu ala glu arg leu ser
91/31

```

31/95

121/41 151/51
GAT GAA GAC CTT TTC AAG TTT CTG GCC GAC ATG CGG CGA CCA TCA TCC CTG CTG AGG CGA
asp glu asp leu phe lys phe leu ala asp met arg arg pro ser ser leu leu arg arg
181/61 211/71
TTG CGC CCT GTG ACA GCT CAG CTC AAG CTT GAC ATC TCC CCG GCC CCC GAG AAC CTG CAC
leu arg pro val thr ala gln leu lys leu asp ile ser pro ala pro glu asn leu his
241/81 271/91
TTC TGC CTG TCC CCT GAC TTA CTT CAT GTC AAG CCC TAC CCT GAC CCC AGG GGA CGG CCC
phe cys leu ser pro asp leu leu his val lys pro tyr pro asp pro arg gly arg pro
301/101 331/111
ACC AAG GAG ATC CTG GAG TTC CCT GCC CGC GAG GTC TAC GCC CCC CAT TCC TGT TAC AGG
thr lys glu ile leu glu phe pro ala arg glu val tyr ala pro his ser cys tyr arg
361/121 391/131
AAC CTG CTC TTC GTG TAC CCA CAC AGC CTC AAT TTC AGC AGT CGC CAG GGC TCT GTG CGC
asn leu leu phe val tyr pro his ser leu asn phe ser ser arg gln gly ser val arg
421/141 451/151
AAC CTG GCT GTG CGG ATC CAG TAC ATG GCC GGT GAA GAC CAG AGC CAG GCC TTG CCG GTC
asn leu ala val arg ile gln tyr met ala gly glu asp gln ser gln ala leu pro val
481/161 511/171
ATC TTT GGG AAA TCT AGC TGC AGC GAA TTC ACC CGA GAG GCC TTC ACA CCA GTG GTC TAT
ile phe gly lys ser ser cys ser glu phe thr arg glu ala phe thr pro val val tyr
541/181 571/191
CAC AAC AAG TCT CCT GAA TTC TAC GAG GAA TTC AAG CTA CGA CTT CCT GCC TGC GTG ACC
his asn lys ser pro glu phe tyr glu glu phe lys leu arg leu pro ala cys val thr
601/201 631/211
GAG AAC CAT CAC CTC TTT TTT ACC TTC TAC CAT GTC AGC TGC CAG CCC CGG CCA GGA ACA
glu asn his his leu phe phe thr phe tyr his val ser cys gln pro arg pro gly thr
661/221 691/231
GCC TTG GAG ACG CCT GTG GGC TTC ACT TGG ATC CCT CTG TTA CAA CAT GGC CGC CTG AGG
ala leu glu thr pro val gly phe thr trp ile pro leu leu gln his gly arg leu arg
721/241 751/251
ACT GGT CCC TTC TGC CTG CCC GTG TCC GTG GAC CAG CCT CCA CCC AGC TAC TCG GTC CTG
thr gly pro phe cys leu pro val ser val asp gln pro pro pro ser tyr ser val leu
781/261 811/271
ACC CCA GAT GTA GCG CTG CCT GGC ATG CGC TGG GTG GAC GGC CAC AAG GGC GTG TTC AGT
thr pro asp val ala leu pro gly met arg trp val asp gly his lys gly val phe ser
841/281 871/291
GTG GAG CTC ACC GCC GTG TCG TCC GTG CAC CCG CAG GAC CCC CAC TTG GAT AAG TTC TTC
val glu leu thr ala val ser ser val his pro gln asp pro his leu asp lys phe phe
901/301 931/311
ACG CTG GTA CAT GTT CTA GAG GAA GGG ATC TTT CCG TTC CGA CTC AAG GAG ACA GTG CTG
thr leu val his val leu glu glu gly ile phe pro phe arg leu lys glu thr val leu
961/321 991/331
AGC GAA GGC ACT ATG GAG CAG GAG TTG CGA GCC AGC CTG GCA GCC CTG CGC CTT GCC AGC
ser glu gly thr met glu gln glu leu arg ala ser leu ala ala leu arg leu ala ser
1021/341 1051/351
CCA GAG CCC CTA GTA GCC TTT TCC CAC CTC GTG CTA GAC AAG CTT GTC CGC TTG GTT GTG
pro glu pro leu val ala phe ser his leu val leu asp lys leu val arg leu val val

16
Figure X (31 of 35)

32/95

```

1081/361                                1111/371
CGG CCA CCC ATC ATT TGT GGC CAG ATG GTG AAC CTG GGT CGA GGG GCC TTT GAA GCT ATG
arg pro pro ile ile cys gly gln met val asn leu gly arg gly ala phe glu ala met
1141/381                                1171/391
GCT CAT GTA GCC AGC CTT GTG CAC CGG AAC CTG GAG GCT GTC CAA GAC TCC CGT GGC CAC
ala his val ala ser leu val his arg asn leu glu ala val gln asp ser arg gly his
1201/401                                1231/411
TGC CCA CTG CTG GCC TCC TAT GTC CAC TAC GCC TTT CGC CTC CCT GGT GGT GAC CTC AGC
cys pro leu leu ala ser tyr val his tyr ala phe arg leu pro gly gly asp leu ser
1261/421                                1291/431
CTG CCA GGC GAA GCC CCT CCA GCA ACT GTG CAG GCT GCC ACA CTG GCC CGT GGC TCT GGT
leu pro gly glu ala pro pro ala thr val gln ala ala thr leu ala arg gly ser gly
1321/441                                1351/451
CGC CCC GCC AGC CTG TAC CTG GCA CGG TCT AAG AGC ATC AGC AGC AGC AAC CCT GAC CTG
arg pro ala ser leu tyr leu ala arg ser lys ser ile ser ser ser asn pro asp leu
1381/461                                1411/471
GCT GTG GTC CCT GGC TCT GTG GAC GAT GAG GTG TCC CGC ATC CTA GCC AGC AAG GGT GTC
ala val val pro gly ser val asp asp glu val ser arg ile leu ala ser lys gly val
1441/481                                1471/491
GAT CGC TCA CAC TCC TGG GTG AAT TCT GCT TAT GCT CCG GGA GGC AGC AAG GCT GTG CTG
asp arg ser his ser trp val asn ser ala tyr ala pro gly gly ser lys ala val leu
1501/501                                1531/511
CGG CGG GTG CCC CCA TAC TGT GGG GCT GAT CCC AGA CAG CTG CTG CAC GAG GAG CTG GCT
arg arg val pro pro tyr cys gly ala asp pro arg gln leu leu his glu glu leu ala
1561/521
CTG CAG TGG GTG GTG AGC GGC AGT GCG GTT
leu gln trp val val ser gly ser ala val

```

2. mouse CLASP-7 cDNA fragment 2

```

1/1                                31/11
ATG GTA AAA AGC ATG GAG CTC CAT CTG CTT CTG GGC CAG CGA CTG GAC ACT CCC CGC AAG
Met val lys ser met glu leu his leu leu leu gly gln arg leu asp thr pro arg lys
61/21                                91/31
CTG CGC TTC CCT GGG CGC TTC CTG GAT GAC ATT GCC GCC CTG GTG GCT TCC GTG GGC CTG
leu arg phe pro gly arg phe leu asp asp ile ala ala leu val ala ser val gly leu
121/41                                151/51
GAA GTC ATC ACC AGA GTC CAT AAG GAC ATG AAG CTA GCT GAA CGC CTC AAC GCT AGC CTG
glu val ile thr arg val his lys asp met lys leu ala glu arg leu asn ala ser leu
181/61                                211/71
GCT TTC TTC CTC AGT GAC CTC CTG TCC ATA GCG GAC CGA GGC TAC ATT TTC AGC CTG GTA
ala phe phe leu ser asp leu leu ser ile ala asp arg gly tyr ile phe ser leu val
241/81                                271/91
CGC GCT CAC TAC AAG CAG GTG GCC ACT CGG CTC CAG TCT GCC CCC AAC CCA ACT GCA CTG
arg ala his tyr lys gln val ala thr arg leu gln ser ala pro asn pro thr ala leu
301/101                                331/111
CTC ACA CTA CGA ATG GAC TTC ACC CGC ATC CTG TGT AGC CAT GAG CAC TAT GTG ACC CTT
leu thr leu arg met asp phe thr arg ile leu cys ser his glu his tyr val thr leu

```

16

Figure 1 (32 of 35)

33/95

```

361/121                               391/131
AAC CTC CCC TGT TGC CCC CTG TCG CCC CCA GCA TCC CCG TCC CCC TCG GTG TCC TCC ACT
asn leu pro cys cys pro leu ser pro pro ala ser pro ser pro ser val ser ser thr
421/141                               451/151
ACC TCC CAG AGC TCC ACC TTC TCC AGC CAG GCC CCC GAT CCG AAG GTG ACC AGC ATG TTC
thr ser gln ser ser thr phe ser ser gln ala pro asp pro lys val thr ser met phe
481/161                               511/171
GAG CTG AGC GGG CCC TTC AGG CAG CAG CAC TTC CTG TCC GGA CTC CTG CTG ACA GAG CTG
glu leu ser gly pro phe arg gln gln his phe leu ser gly leu leu leu thr glu leu
541/181                               571/191
GCC CTG GCC CTG GAT CCG GAA GCT GAG GGG GCA TCC CTT TTG CAC AAG AAG GCT ATT AGT
ala leu ala leu asp pro glu ala glu gly ala ser leu leu his lys lys ala ile ser
601/201                               631/211
GCC GTG CAC AGC CTG CTG TGC AGC CAC GAT GTT GAC TCC CGC TAC GCA GAA GCT ACC GTG
ala val his ser leu leu cys ser his asp val asp ser arg tyr ala glu ala thr val
661/221                               691/231
AAC GCC AAG GTG GCC GAG CTG TAC CTG CCC CTC CTC TCC CTT
asn ala lys val ala glu leu tyr leu pro leu leu ser leu

```

3. mouse CLASP-7 cDNA fragment 3

```

1/1                               31/11
GAA ATG GAA CAT GAA GCT CTG GTG GAC GGA AAC CTG GCG ACA GAG GCC AGC CTG GTG GTT
glu met glu his glu ala leu val asp gly asn leu ala thr glu ala ser leu val val
61/21                               91/31
CTG GAC ACG CTG GAG ACC ATC GTG CAG ACA GTG ATG CTG TCC GAG GCC CGT GAG AGC ATC
leu asp thr leu glu thr ile val gln thr val met leu ser glu ala arg glu ser ile
121/41                               151/51
CTG AGT GCC GTG CTG AAA GTT GTC CTC TAC AGT CTT GGG AGC GCC CAG AGT GCC CTG TTC
leu ser ala val leu lys val val leu tyr ser leu gly ser ala gln ser ala leu phe
181/61                               211/71
CTG CAG CAT GGC CTG GCC ACC CAG CGG GCC CTG GTC TCC AAG TTT CCG GAG CTG CTT TTC
leu gln his gly leu ala thr gln arg ala leu val ser lys phe pro glu leu leu phe
241/81                               271/91
GAG GAA GAC ACG GAG CTT TGT GCC GAC CTG TGC CTG AGA CTT CTG CGA CAC TGT GGC AGC
glu glu asp thr glu leu cys ala asp leu cys leu arg leu leu arg his cys gly ser
301/101                               331/111
CGC ATC AGC ACC ATC CGC ATG CAC GCC AGC GCC TCC CTC TAC CTG CTT ATG CGC CAG AAC
arg ile ser thr ile arg met his ala ser ala ser leu tyr leu leu met arg gln asn
361/121                               391/131
TTC GAG ATT GGC CAT AAC TTT GCC CGT GTG AAG ATG CTG GTG ACC ATG TCT CTG TCG TCC
phe glu ile gly his asn phe ala arg val lys met leu val thr met ser leu ser ser
421/141                               451/151
CTT GTG GGG ACA ACT CAG AAC TTT AGT GAA GAG CAT TTG AGA AAG TCC CTC AAG ACC ATC
leu val gly thr thr gln asn phe ser glu glu his leu arg lys ser leu lys thr ile
481/161                               511/171
CTG ACC TAC GCA GAG GAG GAC ATA GGG CTG AGG GAC AGC ACC TTC GCT GAG CAG GTC CAG
leu thr tyr ala glu glu asp ile gly leu arg asp ser thr phe ala glu gln val gln

```

541/181
 GAC CTC ATG TTC AAC CTG CAC ATG ATC CTG ACA GAC ACG GTG AAG ATG AAG GAA CAC CAG
 asp leu met phe asn leu his met ile leu thr asp thr val lys met lys glu his gln
 601/201
 GAG GAC CCT GAG ATG CTC ATG GAC CTC ATG TAC AGA ATT GCT CGG GGA TAC CAA GGC TCT
 glu asp pro glu met leu met asp leu met tyr arg ile ala arg gly tyr gln gly ser
 661/221
 CCA GAC CTG CGG CTG ACA TGG CTG CAG AAC ATG GCT GGC AAA CAT GCA GAG CTG GGC AAT
 pro asp leu arg leu thr trp leu gln asn met ala gly lys his ala glu leu gly asn
 721/241
 CAT GCA GAG GCT GCC CAG TGC ATG GTC CAC GCC GCT GCC CTG GTG GCC GAA TAC CTT GCC
 his ala glu ala ala gln cys met val his ala ala ala leu val ala glu tyr leu ala
 781/261
 CTC CTC GAG GAC AGT CGC CAC CTG CCT GTG GGC TGT GTG TCC TTC CAG AAT GTC TCA TCC
 leu leu glu asp ser arg his leu pro val gly cys val ser phe gln asn val ser ser
 841/281
 AAC GTG CTG GAG GAG TCT GCC ATC TCT GAT GAC ATC CTG TCG CCA GAT GAG GAG GGC TTC
 asn val leu glu glu ser ala ile ser asp asp ile leu ser pro asp glu glu gly phe
 901/301
 TGC TCT GGG AAG AAC TTC ACA GAA CTG GGT CTG GTG GGG CTG CTG GAG CAG GCG GCC GGC
 cys ser gly lys asn phe thr glu leu gly leu val gly leu leu glu gln ala ala gly
 961/321
 TAC TTC ACC ATG GGT GGT CTG TAT GAA GCG GTG AAC GAA GTC TAC AAA AAC CTT ATC CCC
 tyr phe thr met gly gly leu tyr glu ala val asn glu val tyr lys asn leu ile pro
 1021/341
 ATC CTT GAA GCC CAC AGA GAC TAC AAG AAG CTG GCT GCG GTG CAC GGG AAA CTG CAG GAG
 ile leu glu ala his arg asp tyr lys lys leu ala ala val his gly lys leu gln glu
 1081/361
 GCC TTC ACC AAG ATT ATG CAC CAG AGC TCT GGC TGG GAG CGT GTA TTT GGG ACA TAT TTC
 ala phe thr lys ile met his gln ser ser gly trp glu arg val phe gly thr tyr phe
 1141/381
 CGA GTG GGC TTC TAT GGC ACA CGA TTT GGT GAC CTG GAT GAA CAA GAG TTT GTG TAC AAG
 arg val gly phe tyr gly thr arg phe gly asp leu asp glu gln glu phe val tyr lys
 1201/401
 GAA CCG TCA ATC ACG AAG CTT GCA GAG ATC TCA CAC CGG CTG GAG GAG TTC TAT ACG GAA
 glu pro ser ile thr lys leu ala glu ile ser his arg leu glu glu phe tyr thr glu
 1261/421
 AGG TTC GGG GAT GAT GTG GTA GAG ATC ATC AAA GAT TCT AAC CCA GTG GAC AAG TCC AAG
 arg phe gly asp asp val val glu ile ile lys asp ser asn pro val asp lys ser lys
 1321/441
 CTG GAC CCA CAG AAG GCG TAC ATA CAG ATA ACC TAT GTG GAG CCA CAT TTC GAC ACT TAT
 leu asp pro gln lys ala tyr ile gln ile thr tyr val glu pro his phe asp thr tyr
 1381/461
 GAG CTC AAG GAT CGG GTG ACC TAC TTC GAT CGG AAC TAT GGG CTG CGG GCC TTC CTC TTC
 glu leu lys asp arg val thr tyr phe asp arg asn tyr gly leu arg ala phe leu phe
 1441/481
 TGC ACA CCC TTC ACA CCA GAT GGA CGT GCG CAC GGA GAG TTG GCC GAA CAG CAC AAA CGC
 cys thr pro phe thr pro asp gly arg ala his gly glu leu ala glu gln his lys arg

35/95

```
1501/501                                1531/511
AAG ACG CTG CTG AGC ACG GAG CAT GCC TTT CCC TAC ATC AAG ACA CGC ATC CGA GTG TGC
lys thr leu leu ser thr glu his ala phe pro tyr ile lys thr arg ile arg val cys
1561/521                                1591/531
CAC CGT GAG GAG ACA GTG CTG ACA CCA GTG GAG GTG GCC ATT GAG GAC ATG CAG AAG AAG
his arg glu glu thr val leu thr pro val glu val ala ile glu asp met gln lys lys
1621/541                                1651/551
ACC CGG GAG CTG GCC TTT GCC ACC GAG CAG GAC CCT CCA GAT GCC AAG ATG CTG CAG ATG
thr arg glu leu ala phe ala thr glu gln asp pro pro asp ala lys met leu gln met
1681/561                                1711/571
GTT CTC CAG GGT TCT GTG GGA CCC ACT GTG AAC CAG GGT CCC TTG GAA GTG GCC CAG GTG
val leu gln gly ser val gly pro thr val asn gln gly pro leu glu val ala gln val
1741/581                                1771/591
TTT TTG TCA GAG ATC CCA GAA GAT CCC AAG CTC TTC CGA CAT CAC AAC AAA CTC CGG CTC
phe leu ser glu ile pro glu asp pro lys leu phe arg his his asn lys leu arg leu
1801/601                                1831/611
TGC TTC AAG GAT TTC TGC AAA AAG TGC GAG GAT GCA CTG AGA AAG AAC AAG GCC CTG ATT
cys phe lys asp phe cys lys lys cys glu asp ala leu arg lys asn lys ala leu ile
1861/621                                1891/631
GGC CCA GAC CAG AAG GAG TAC CAC CGG GAG CTG GAG CGT CAC TAT AGC CGC CTG CGG GAG
gly pro asp gln lys glu tyr his arg glu leu glu arg his tyr ser arg leu arg glu
1921/641                                1951/651
GCT CTG CAG CCT CTG CTT ACC CAA CGT CTG CCC CAG CTG CTG GCA CCA AGT TCC ACC AGC
ala leu gln pro leu leu thr gln arg leu pro gln leu leu ala pro ser ser thr ser
1981/661                                2011/671
CTC AGG AGC TCC ATG AAC AGA TCA AGT TTC AGG AAG GCT GAC CTC TGA CAA GGC TAA GAG
leu arg ser ser met asn arg ser ser phe arg lys ala asp leu OPA

2041/681                                2071/691
CCA CAC CCA GAA GAC CAG CAC CCA CAC TGA AAA
```

-21

GTCGCCGTCGCCGAGCAGCC -1

1/1	31/11
ATG GCC GAG CGC CGC GCC TTC GCC CAG AAG	ATC AGC AGA ACG GTG GCA GCC GAA GTT AGG
Met ala glu arg arg ala phe ala gln lys	ile ser arg thr val ala ala glu val arg
61/21	91/31
AAG CAG ATC TCC GGA CAA TAT AGT GGT TCT	CCC CAA CTG CTC AAA AAC CTT AAT ATT GTT
lys gln ile ser gly gln tyr ser gly ser	pro gln leu leu lys asn leu asn ile val
121/41	151/51
GGC AAT ATA TCC CAT CAC ACC ACA GTG CCC	CTT ACC GAA GCA GTA GAT CCA GTG GAT TTG
gly asn ile ser his his thr thr val pro	leu thr glu ala val asp pro val asp leu
181/61	211/71
GAA GAT TAC CTC ATT ACT CAT CCT TTG GCT	GTG GAT TCT GGG CCT TTA CGG GAT TTG ATT
glu asp tyr leu ile thr his pro leu ala	val asp ser gly pro leu arg asp leu ile
241/81	271/91
GAA TTT CCT CCA GAT GAT ATT GAA GTT GTT	TAT AGT CCT CGG GAC TGC AGA ACT CTT GTT
glu phe pro pro asp asp ile glu val val	tyr ser pro arg asp cys arg thr leu val
301/101	331/111
TCA GCT GTA CCT GAA GAA AGT GAA ATG GAT	CCA CAT GTT AGA GAC TGT ATA AGA AGT TAT
ser ala val pro glu glu ser glu met asp	pro his val arg asp cys ile arg ser tyr
361/121	391/131
ACA GAA GAC TGG GCA ATT GTC ATC AGA AAA	TAT CAT AAA TTG GGA ACA GGA TTT AAT CCC
thr glu asp trp ala ile val ile arg lys	tyr his lys leu gly thr gly phe asn pro
421/141	451/151
AAT ACA TTA GAT AAA CAG AAA GAA AGG CAA	AAA GGT TTG CCA AAA CAA GTT TTT GAA TCT
asn thr leu asp lys gln lys glu arg gln	lys gly leu pro lys gln val phe glu ser
481/161	511/171
GAT GAA GCT CCA GAT GGC AAC AGC TAC CAG	GAT GAT CAA GAT GAC CTT AAA AGA CGT TCA
asp glu ala pro asp gly asn ser tyr gln	asp asp gln asp asp leu lys arg arg ser
541/181	571/191
ATG TCA ATA GAT GAT ACC CCA AGG GGT AGC	TGG GCC TGT AGT ATC TTT GAC TTG AAA AAT
met ser ile asp asp thr pro arg gly ser	trp ala cys ser ile phe asp leu lys asn
601/201	631/211
TCA CTT CCT GAT GCT TTG CTT CCC AAT TTA	CTT GAT CGA ACT CCA AAT GAA GAA ATA GAC
ser leu pro asp ala leu leu pro asn leu	leu asp arg thr pro asn glu glu ile asp
661/221	691/231
CGT CAG AAT GAT GAC CAA AGG AAA TCA AAC	CGT CAC AAA GAA CTT TTT GCT TTG CAT CCA
arg gln asn asp asp gln arg lys ser asn	arg his lys glu leu phe ala leu his pro
721/241	751/251
TCA CCA GAT GAG GAA GAA CCA ATA GAA CGG	CTT AGT GTT CCT GAT ATA CCC AAA GAA CAT
ser pro asp glu glu glu pro ile glu arg	leu ser val pro asp ile pro lys glu his
781/261	811/271
TTT GGT CAA AGA CTT CTT GTA AAA TGC TTA	TCA CTC AAG TTT GAA ATT GAA ATT GAA CCC
phe gly gln arg leu leu val lys cys leu	ser leu lys phe glu ile glu ile glu pro
841/281	871/291
ATT TTT GCA AGT TTG GCT TTA TAT GAT GTC	AAG GAA AAG AAA AAG ATT TCA GAA AAC TTT
ile phe ala ser leu ala leu tyr asp val	lys glu lys lys lys ile ser glu asn phe
901/301	931/311
TAT TTT GAC CTT AAT TCT GAG CAG ATG AAA	GGG TTG TTA CGT CCA CAT GTA CCA CCT GCT
tyr phe asp leu asn ser glu gln met lys	gly leu leu arg pro his val pro pro ala
961/321	991/331
GCC ATT ACT ACC CTG GCA AGA TCA GCA ATT	TTT TCT ATC ACT TAT CCT TCC CAA GAT GTT
ala ile thr thr leu ala arg ser ala ile	phe ser ile thr tyr pro ser gln asp val

1021/341	TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA	1051/351	CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
phe leu val ile lys leu glu lys val leu	1081/361	1111/371	gln gln gly asp ile gly glu cys ala glu
CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC	1141/381	1171/391	thr lys asn lys glu lys leu glu lys leu
pro tyr met ile phe lys glu ala asp ala	AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA	1231/411	CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
lys ser gln ala asp gln phe cys gln arg	1201/401	1291/431	leu gly lys tyr arg met pro phe ala trp
ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC	1261/421	1351/451	AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
thr ala ile his leu met asn ile val ser	GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA	1411/471	ser ala gly ser leu glu arg asp ser thr
glu val glu ile ser thr gly glu arg lys	1321/441	1471/491	GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA	1381/461	1531/511	ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
ile val gly arg arg ser leu glu arg thr	AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA	1591/531	thr ser gly asp asp ala cys asn leu thr
ser phe arg pro ala thr leu thr val thr	1441/481	1651/551	AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT	1501/501	1711/571	asn phe phe lys gln glu gly asp arg leu
ser asp glu asp leu tyr lys phe leu ala	CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG	1771/591	GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
arg leu arg pro ile thr ala gln leu lys	1561/521	1831/611	asp met arg arg pro ser ser val leu arg
CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA	1621/541	1891/631	ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
his tyr cys leu thr pro glu leu leu gln	CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA	1951/651	ile asp ile ser pro ala pro glu asn pro
pro thr arg glu ile leu glu phe pro ala	1681/561	2011/671	GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT	1741/581	2071/691	val lys leu tyr pro asp ser arg val arg
arg asn leu leu tyr ile tyr pro gln ser	AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG	2131/711	AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG	1801/601		arg asp val tyr val pro asn thr thr tyr
arg asn ile thr val lys val gln phe met	GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA		CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
val ile phe gly lys ser ser cys ser glu	1861/621		leu asn phe ala asn arg gln gly ser ala
TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA	1921/641		leu asn phe ala asn arg gln gly ser ala
tyr his asn arg ser pro asp phe his glu	ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT		TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
thr asp his his his leu leu phe thr phe	1981/661		tyr gly glu asp pro ser asn ala met pro
ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA	2041/681		TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
thr pro leu glu thr pro val gly tyr thr	AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA		phe ser lys glu ala tyr thr ala val val
lys thr gly gln phe cys leu pro val ser	2101/701		GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG			glu ile lys val lys leu pro ala thr leu
leu ser pro glu val pro leu pro gly met			tyr his val ser cys gln gln lys gln asn
			lys trp val asp asn his lys gly val phe

2161/721	2191/731
AAT GTT GAA GTT GTT GCT GTT TCG TCT ATC	CAT ACA CAA GAT CCT TAT CTT GAC AAA TTT
asn val glu val val ala val ser ser ile	his thr gln asp pro tyr leu asp lys phe
2221/741	2251/751
TTT GCT CTG GTC AAT GCT CTG GAT GAA CAC	CTG TTC CCA GTC CGA ATT GGG GAC ATG CGA
phe ala leu val asn ala leu asp glu his	leu phe pro val arg ile gly asp met arg
2281/761	2311/771
ATC ATG GAA AAT AAC TTA GAA AAT GAA TTG	AAG AGC AGT ATT TCA GCA CTG AAT TCA TCC
ile met glu asn asn leu glu asn glu leu	lys ser ser ile ser ala leu asn ser ser
2341/781	2371/791
CAG CTG GAA CCA GTG GTC CGA TTT CTT CAT	CTT CTG CTA GAT AAA CTG ATA CTT TTA GTT
gln leu glu pro val val arg phe leu his	leu leu leu asp lys leu ile leu leu val
2401/801	2431/811
ATT AGA CCT CCT GTC ATT GCT GGC CAA ATA	GTT AAC CTA GGT CAA GCA TCT TTT GAA GCC
ile arg pro pro val ile ala gly gln ile	val asn leu gly gln ala ser phe glu ala
2461/821	2491/831
ATG GCA TCA ATT ATA AAT CGA CTT CAC AAA	AAC TTG GAA GGA AAT CAT GAC CAG CAT GGC
met ala ser ile ile asn arg leu his lys	asn leu glu gly asn his asp gln his gly
2521/841	2551/851
AGA AAC AGC CTT CTT GCA TCA TAT ATT CAT	TAT GTT TTC CGC CTA CCA AAT ACT TAC CCT
arg asn ser leu leu ala ser tyr ile his	tyr val phe arg leu pro asn thr tyr pro
2581/861	2611/871
AAT TCA TCA TCA CCA GGT CCT GGG GGT TTG	GGA GGA TCA GTG CAT TAT GCC ACA ATG GCT
asn ser ser ser pro gly pro gly gly leu	gly gly ser val his tyr ala thr met ala
2641/881	2671/891
AGA TCT GCG GTG AGA CCT GCA AGC CTT AAT	TTA AAT CGT TCT CGA AGC CTT AGT AAT AGC
arg ser ala val arg pro ala ser leu asn	leu asn arg ser arg ser leu ser asn ser
2701/901	2731/911
AAT CCA GAT ATA TCT GGG ACT CCC ACG TCA	CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG
asn pro asp ile ser gly thr pro thr ser	pro asp asp glu val arg ser ile ile gly
2761/921	2791/931
AGT AAG GGT TTA GAT CGC TCC AAT TCC TGG	GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA
ser lys gly leu asp arg ser asn ser trp	val asn thr gly gly pro lys ala ala pro
2821/941	2851/951
TGG GGA TCC AAC CCC AGT CCA AGT GCA GAA	TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT
trp gly ser asn pro ser pro ser ala glu	ser thr gln ala met asp arg ser cys asn
2881/961	2911/971
CGT ATG TCT TCG CAC ACA GAG ACG TCA AGT	TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA
arg met ser ser his thr glu thr ser ser	phe leu gln thr leu thr gly arg leu pro
2941/981	2971/991
ACT AAA AAG CTT TTT CAC GAG GAG CTG GCT	TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT
thr lys lys leu phe his glu glu leu ala	leu gln trp val val cys ser gly ser val
3001/1001	3031/1011
CGG GAA TCA GCT TTG CAA CAA GCC TGG TTC	TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG
arg glu ser ala leu gln gln ala trp phe	phe phe glu leu met val lys ser met val
3061/1021	3091/1031
CAC CAT TTA TAC TTT AAT GAT AAA CTT GAG	GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT
his his leu tyr phe asn asp lys leu glu	ala pro arg lys ser arg phe pro glu arg
3121/1041	3151/1051
TTC ATG GAT GAC ATT GCA GCT CTT GTC AGC	ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT
phe met asp asp ile ala ala leu val ser	thr ile ala ser asp ile val ser arg phe
3181/1061	3211/1071
CAG AAG GAC ACA GAA ATG GTT GAG AGA CTC	AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT
gln lys asp thr glu met val glu arg leu	asn thr ser leu ala phe phe leu asn asp
3241/1081	3271/1091
CTG TTG TCT GTT ATG GAC AGA GGA TTT GTT	TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG
leu leu ser val met asp arg gly phe val	phe ser leu ile lys ser cys tyr lys gln

3301/1101	3331/1111
GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT	CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT
val ser ser lys leu tyr ser leu pro asn	pro ser val leu val ser leu arg leu asp
3361/1121	3391/1131
TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC	TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA
phe leu arg ile ile cys ser his glu his	tyr val thr leu asn leu pro cys ser leu
3421/1141	3451/1151
CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT	GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA
leu thr pro pro ala ser pro ser pro ser	val ser ser ala thr ser gln ser ser gly
3481/1161	3511/1171
TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT	GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC
phe ser thr asn val gln asp gln lys ile	ala asn met phe glu leu ser val pro phe
3541/1181	3571/1191
CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG	TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT
arg gln gln his tyr leu ala gly leu val	leu thr glu leu ala val ile leu asp pro
3601/1201	3631/1211
GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG	AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC
asp ala glu gly leu phe gly leu his lys	lys val ile asn met val his asn leu leu
3661/1221	3691/1231
TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT	GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG
ser ser his asp ser asp pro arg tyr ser	asp pro gln ile lys ala arg val ala met
3721/1241	3751/1251
TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG	GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA
leu tyr leu pro leu ile gly ile ile met	glu thr val pro gln leu tyr asp phe thr
3781/1261	3811/1271
GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT	TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG
glu thr his asn gln arg gly arg pro ile	cys ile ala thr asp asp tyr glu ser glu
3841/1281	3871/1291
AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC	ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA
ser gly ser met ile ser gln thr val ala	met ala ile ala gly thr ser val pro gln
3901/1301	3931/1311
CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG	TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT
leu thr arg pro gly ser phe leu leu thr	ser thr ser gly arg gln his thr thr phe
3961/1321	3991/1331
TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC	TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT
ser ala glu ser ser arg ser leu leu ile	cys leu leu trp val leu lys asn ala asp
4021/1341	4051/1351
GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT	CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA
glu thr val leu gln lys trp phe thr asp	leu ser val leu gln leu asn arg leu leu
4081/1361	4111/1371
GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT	GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA
asp leu leu tyr leu cys val ser cys phe	glu tyr lys gly lys lys val phe glu arg
4141/1381	4171/1391
ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA	GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT
met asn ser leu thr phe lys lys ser lys	asp met arg ala lys leu glu glu ala ile
4201/1401	4231/1411
CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG	GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA
leu gly ser ile gly ala arg gln glu met	val arg arg ser arg gly gln leu glu arg
4261/1421	4291/1431
AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA	GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT
ser pro ser gly ser ala phe gly ser gln	glu asn leu arg trp arg lys asp met thr
4321/1441	4351/1451
CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC	AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA
his trp arg gln asn thr glu lys leu asp	lys ser arg ala glu ile glu his glu ala
4381/1461	4411/1471
CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA	AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT
leu ile asp gly asn leu ala thr glu ala	asn leu ile ile leu asp thr leu glu ile

4441/1481	4471/1491
GTT GTT CAG ACC GTT TCT GTA ACG GAA TCC	AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA
val val gln thr val ser val thr glu ser	lys glu ser ile leu gly gly val leu lys
4501/1501	4531/1511
GTG CTA CTA CAC AGC ATG GCC TGT AAC CAA	AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT
val leu leu his ser met ala cys asn gln	ser ala val tyr leu gln his cys phe ala
4561/1521	4591/1531
ACA CAG AGA GCC TTG GTT TCA AAG TTT CCT	GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG
thr gln arg ala leu val ser lys phe pro	glu leu leu phe glu glu glu thr glu gln
4621/1541	4651/1551
TGT GCT GAT TTA TGC CTC AGG CTT CTC CGA	CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG
cys ala asp leu cys leu arg leu leu arg	his cys ser ser ser ile gly thr ile arg
4681/1561	4711/1571
TCA CAC CCC AGT GCC TCC CTT TAC CTA CTA	ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC
ser his pro ser ala ser leu tyr leu leu	met arg gln asn phe glu ile gly asn asn
4741/1581	4771/1591
TTT GCC AGG GTT AAA ATG CAG GTA CCA ATG	TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG
phe ala arg val lys met gln val pro met	ser leu ser ser leu val gly thr ser gln
4801/1601	4831/1611
AAT TTT AAT GAA GAA TTC TTA AGA CGT TCT	CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA
asn phe asn glu glu phe leu arg arg ser	leu lys thr ile leu thr tyr ala glu glu
4861/1621	4891/1631
GAT CTG GAA TTG AGG GAA ACA ACA TTT CCT	GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC
asp leu glu leu arg glu thr thr phe pro	asp gln val gln asp leu val phe asn leu
4921/1641	4951/1651
CAT ATG ATT CTT TCT GAT ACT GTG AAA ATG	AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG
his met ile leu ser asp thr val lys met	lys glu his gln glu asp pro glu met leu
4981/1661	5011/1671
ATT GAT CTA ATG TAC AGA ATT GCC AAG GGT	TAC CAG ACC TCT CCA GAG CGA TTG ACC TGG
ile asp leu met tyr arg ile ala lys gly	tyr gln thr ser pro glu arg leu thr trp
5041/1681	5071/1691
TTG CAG AAC ATG GCA GGC AAG CAC TCA GAA	CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT
leu gln asn met ala gly lys his ser glu	arg ser asn his ala glu ala ala gln cys
5101/1701	5131/1711
CTA GTC CAC TCA GCA GCA CTT GTT GCT GAA	TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT
leu val his ser ala ala leu val ala glu	tyr leu ser met leu glu asp arg lys tyr
5161/1721	5191/1731
CTT CCT GTG GGA TGT GTA ACA TTT CAG AAT	ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG
leu pro val gly cys val thr phe gln asn	ile ser ser asn val leu glu glu ser ala
5221/1741	5251/1751
GTC TCA GAT GAT GTG GTA TCT CCA GAT GAA	GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT
val ser asp asp val val ser pro asp glu	glu gly ile cys ser gly lys tyr phe thr
5281/1761	5311/1771
GAG TCA GGA CTT GTG GGA TTA CTG GAA CAA	GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG
glu ser gly leu val gly leu leu glu gln	ala ala ala ser phe ser met ala gly met
5341/1781	5371/1791
TAT GAA GCA GTT AAT GAA GTT TAC AAA GTA	CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT
tyr glu ala val asn glu val tyr lys val	leu ile pro ile his glu ala asn arg asp
5401/1801	5431/1811
GCA AAG AAA CTA TCC ACA ATT CAT GGT AAA	CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT
ala lys lys leu ser thr ile his gly lys	leu gln glu ala phe ser lys ile val his
5461/1821	5491/1831
CAG AGT ACT GGC TGG GAG CGG ATG TTT GGC	ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC
gln ser thr gly trp glu arg met phe gly	thr tyr phe arg val gly phe tyr gly thr
5521/1841	5551/1851
AAG TTC GGG GAT TTG GAT GAA CAA GAA TTT	GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT
lys phe gly asp leu asp glu gln glu phe	val tyr lys glu pro ala ile thr lys leu

5581/1861	5611/1871
GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT	TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
ala glu ile ser his arg leu glu gly phe	tyr gly glu arg phe gly glu asp val val
5641/1881	5671/1891
GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC	AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
glu val ile lys asp ser asn pro val asp	lys cys lys leu asp pro asn lys ala tyr
5701/1901	5731/1911
ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT	GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
ile gln ile thr tyr val glu pro tyr phe	asp thr tyr glu met lys asp arg ile thr
5761/1921	5791/1931
TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA	TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
tyr phe asp lys asn tyr asn leu arg arg	phe met tyr cys thr pro phe thr leu asp
5821/1941	5851/1951
GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA	TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
gly arg ala his gly glu leu his glu gln	phe lys arg lys thr ile leu thr thr ser
5881/1961	5911/1971
CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC	AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
his ala phe pro tyr ile lys thr arg val	asn val thr his lys glu glu ile ile leu
5941/1981	5971/1991
ACA CCA ATT GAA GTT GCT ATT GAG GAC ATG	CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
thr pro ile glu val ala ile glu asp met	gln lys lys thr gln glu leu ala phe ala
6001/2001	6031/2011
ACA CAT CAG GAT CCC GCA GAC CCC AAA ATG	CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC
thr his gln asp pro ala asp pro lys met	leu gln met val leu gln gly ser val gly
6061/2021	6091/2031
ACC ACA GTG AAT CAG GGG CCT TTG GAA GTT	GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT
thr thr val asn gln gly pro leu glu val	ala gln val phe leu ser glu ile pro ser
6121/2041	6151/2051
GAC CCA AAG CTC TTC AGA CAT CAT AAT AAA	CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA
asp pro lys leu phe arg his his asn lys	leu arg leu cys phe lys asp phe thr lys
6181/2061	6211/2071
AGG TGT GAA GAT GCC TTA AGA AAA AAT AAG	AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT
arg cys glu asp ala leu arg lys asn lys	ser leu ile gly pro val gln lys glu tyr
6241/2081	6271/2091
CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA	
gln arg glu leu gly lys leu ser ser pro	OCH

AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCCCTGCCACAGAGATTCC
 TTCAGTCGAATGAGCTTTTCGCAAAATGGATCTCTAAACTGAATGCACTTGTTTTATTTCATCTGCAAGAGCCATGTATTC
 AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATTATTATTTCATTGAAGAATGCAGTG
 GCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGCTATGGTTTCTAATGTTCCGGGTAACAAGCTGTTA
 TCTTTTAAGACATTTTAATGACTCAAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT
 TCACTTTAAGTTTCGTATTTTAAATTTATATCACCATTTATAGATTCAATTTTGACCCATTTTAAATGTAGTAATGCTTA
 TTTTAAAGGTACTAAAAAATATGTGAATGTTTACCTCGTGC GCGCCAGGGCCTC

-12 -1
GACGCGAGGACC

1/1	ATG GCT GCC TCC GAG CGC CGC GCC TTC GCG	31/11	CAC AAG ATC AAC AGG ACG GTG GCC GCA GAG
Met ala ala ser glu arg arg ala phe ala	61/21	91/31	his lys ile asn arg thr val ala ala glu
GTG CGG AAG CAG GTG TCC CGG GAA CGC AGT	121/41	151/51	GCG TCC CCC CAC TCC AGC AGG CGC TGC AGC
val arg lys gln val ser arg glu arg ser	181/61	211/71	gly ser pro his ser ser arg arg cys ser
AGC TCC CTG GGG GTC CCA CTG ACT GAA GTT	241/81	271/91	GTC GAG CCC CTG GAC TTT GAG GAT GTA CTT
ser ser leu gly val pro leu thr glu val	301/101	331/111	val glu pro leu asp phe glu asp val leu
CTG AGC CGG CCA CCA GAT GCT GAG CCC GGG	361/121	391/131	CCC CTC AGG GAC CTG GTA GAA TTC CCA GCT
leu ser arg pro pro asp ala glu pro gly	421/141	451/151	pro leu arg asp leu val glu phe pro ala
GAT GAC TTG GAG CTG CTG CTG CAG CCC CGG	481/161	511/171	GAA TGC CGG ACC ACG GAG CCC GGG ATC CCC
asp asp leu glu leu leu leu gln pro arg	541/181	571/191	glu cys arg thr thr glu pro gly ile pro
AAG GAT GAA AAA CTG GAT GCC CAG GTG AGG	601/201	631/211	GCC GCG GTG GAG ATG TAT ATT GAG GAC TGG
lys asp glu lys leu asp ala gln val arg	661/221	691/231	ala ala val glu met tyr ile glu asp trp
GTC ATT GTC CAC AGA AGG TAT CAG TAC CTG	721/241	751/251	AGT GCA GCA TAC AGC CCC GTC ACC ACA GAC
val ile val his arg arg tyr gln tyr leu	781/261	811/271	ser ala ala tyr ser pro val thr thr asp
ACA CAG CGG GAG CGA CAG AAG GGC CTC CCC	841/281	871/291	CGC CAG GTC TTT GAG CAG GAT GCT TCT GGA
thr gln arg glu arg gln lys gly leu pro	901/301	931/311	arg gln val phe glu gln asp ala ser gly
GAC GAG AGG TCC GGC CCT GAG GAC TCG AAT	961/321	991/331	GAC TCC CGG CGT GGC TCG GGC TCC CCG GAA
asp glu arg ser gly pro glu asp ser asn	1021/341	1051/351	asp ser arg arg gly ser gly ser pro glu
GAC ACC CCT CGA AGC AGT GGT GCC TCT AGC	1081/361	1111/371	ATC TTC GAC CTG AGG AAC CTG GCA GCT GAC
asp thr pro arg ser ser gly ala ser ser			ile phe asp leu arg asn leu ala ala asp
TCA TTG CTG CCC TCT CTG CTA GAG CGG GCG			GCC CCA GAA GAT GTG GAC CGG CGC AAT GAA
ser leu leu pro ser leu leu glu arg ala			ala pro glu asp val asp arg arg asn glu
ACC CTT CGA CGG CAG CAC CGG CCC CCG GCC			CTG CTC ACC CTC TAC CCG GCA CCT GAC GAG
thr leu arg arg gln his arg pro pro ala			leu leu thr leu tyr pro ala pro asp glu
GAT GAA GCC GTG GAA CGC TGT AGC CGC CCA			GAG CCA CCC CGC GAG CAC TTT GGA CAA AGG
asp glu ala val glu arg cys ser arg pro			glu pro pro arg glu his phe gly gln arg
ATC TTG GTC AAG TGT CTG TCG CTC AAG TTC			GAG ATT GAA ATT GAG CCC ATC TTT GGG ATC
ile leu val lys cys leu ser leu lys phe			glu ile glu pro ile phe gly ile
TTG GCT CTG TAT GAT GTG CGG GAG AAA AAG			AAG ATC TCG GAG AAC TTC TAC TTC GAC CTG
leu ala leu tyr asp val arg glu lys lys			lys ile ser glu asn phe tyr phe asp leu
AAC TCG GAC TCC ATG AAG GGG CTG CTT CGG			GCT CAT GGC ACC CAC CCT GCC ATC TCC ACC
asn ser asp ser met lys gly leu leu arg			ala his gly thr his pro ala ile ser thr
CTG GCC CGC TCT GCC ATC TTC TCT GTG ACC			TAC CCC TCA CCT GAC ATC TTC CTG GTC ATC
leu ala arg ser ala ile phe ser val thr			tyr pro ser pro asp ile phe leu val ile
AAG TTG GAG AAG GTG CTT CAG CAA GGG GAC			ATC AGT GAG TGC TGT GAG CCT TAC ATG GTG
lys leu glu lys val leu gln gln gly asp			ile ser glu cys cys glu pro tyr met val

TTG AAA GAA GTG GAC ACA GCC AAG AAC AAA GAG AAG CTA GAG AAG CTG CGC CTG GCG GCC
 leu lys glu val asp thr ala lys asn lys glu lys leu glu lys leu arg leu ala ala
 1141/381 1171/391
 GAG CAG TTC TGC ACC CGC CTG GGC CGC TAC CGC ATG CCC TTC GCC TGG ACG GCC GTG CAC
 glu gln phe cys thr arg leu gly arg tyr arg met pro phe ala trp thr ala val his
 1201/401 1231/411
 TTG GCC AAC ATC GTG AGC AGC GCT GGG CAG CTG GAC CGG GAC TCT GAC TCG GAG GGC GAG
 leu ala asn ile val ser ser ala gly gln leu asp arg asp ser asp ser glu gly glu
 1261/421 1291/431
 CGC CGG CCA GCC TGG ACA GAC CGC CGC CGT CGG GGG CCC CAG GAC CGG GCG AGT AGT GGG
 arg arg pro ala trp thr asp arg arg arg arg gly pro gln asp arg ala ser ser gly
 1321/441 1351/451
 GAC GAC GCC TGC AGC TTC TCT GGC TTC CGT CCA GCC ACG CTA ACT GTC ACA AAC TTC TTT
 asp asp ala cys ser phe ser gly phe arg pro ala thr leu thr val thr asn phe phe
 1381/461 1411/471
 AAG CAG GAG GCT GAG CGA CTC AGT GAC GAG GAC CTC TTC AAG TTC CTG GCT GAC ATG AGG
 lys gln glu ala glu arg leu ser asp glu asp leu phe lys phe leu ala asp met arg
 1441/481 1471/491
 CGC CCG TCG TCC CTG CTG CGG CGA CTA CGT CCT GTG ACT GCC CAG CTC AAG ATC GAC ATT
 arg pro ser ser leu leu arg arg leu arg pro val thr ala gln leu lys ile asp ile
 1501/501 1531/511
 TCT CCG GCT CCT GAA AAT CCC CAC TTC TGC CTC TCC CCT GAG CTG CTT CAT ATC AAG CCC
 ser pro ala pro glu asn pro his phe cys leu ser pro glu leu leu his ile lys pro
 1561/521 1591/531
 TAC CCG GAC CCC AGG GGC CGG CCC ACC AAG GAG ATT CTG GAG TTC CCC GCC CGC GAA GTC
 tyr pro asp pro arg gly arg pro thr lys glu ile leu glu phe pro ala arg glu val
 1621/541 1651/551
 TAT GCC CCC CAT ACC AGC TAC AGG AAC CTG CTG TAC GTG TAC CCG CAC AGC CTC AAC TTC
 tyr ala pro his thr ser tyr arg asn leu leu tyr val tyr pro his ser leu asn phe
 1681/561 1711/571
 AGC AGC CGC CAG GGC TCC GTG CGC AAC CTT GCT GTG CGA GTG CAG TAC ATG ACA GGC GAG
 ser ser arg gln gly ser val arg asn leu ala val arg val gln tyr met thr gly glu
 1741/581 1771/591
 GAC CCC AGC CAG GCT CTG CCG GTC ATC TTT GGC AAG TCC AGC TGC AGT GAA TTT ACC CGC
 asp pro ser gln ala leu pro val ile phe gly lys ser ser cys ser glu phe thr arg
 1801/601 1831/611
 GAG GCC TTC ACA CCG GTG GTC TAC CAT AAC AAG TCC CCC GAG TTC TAC GAG GAG TTC AAG
 glu ala phe thr pro val val tyr his asn lys ser pro glu phe tyr glu glu phe lys
 1861/621 1891/631
 CTG CAT CTT CCA GCC TGC GTG ACA GAG AAC CAT CAC CTG CTG TTC ACC TTC TAC CAT GTC
 leu his leu pro ala cys val thr glu asn his his leu leu phe thr phe tyr his val
 1921/641 1951/651
 AGC TGC CAG CCC CGG CCG GGC ACT GCC CTG GAG ACA CCC GTG GGC TTT ACT TGG ATC CCA
 ser cys gln pro arg pro gly thr ala leu glu thr pro val gly phe thr trp ile pro
 1981/661 2011/671
 CTG CTG CAG CAC GGG CGC CTG AGG ACC GGC CCC TTC TGT CTC CCA GTG TCT GTG GAC CAG
 leu leu gln his gly arg leu arg thr gly pro phe cys leu pro val ser val asp gln
 2041/681 2071/691
 CCG CCG CCC AGC TAT TCC GTG CTC ACA CCC GAT GTG GCG CTT CCG GGC ATG CGC TGG GTG
 pro pro pro ser tyr ser val leu thr pro asp val ala leu pro gly met arg trp val
 2101/701 2131/711
 GAC GGT CAC AAG GGC GTG TTC AGT GTG GAG CTC ACA GCC GTG TCC TCT GTG CAC CCC CAG
 asp gly his lys gly val phe ser val glu leu thr ala val ser ser val his pro gln
 2161/721 2191/731
 GAC CCC TAC CTG GAC AAA TTC TTC ACC CTG GTG CAC GTC CTG GAG GAG GGA GCC TTC CCA
 asp pro tyr leu asp lys phe phe thr leu val his val leu glu glu gly ala phe pro
 2221/741 2251/751
 TTC CGG CTC AAG GAC ACT GTG CTG AGC GAG GGC AAC GTG GAG CAG GAG CTG CGG GCC AGT
 phe arg leu lys asp thr val leu ser glu gly asn val glu gln glu leu arg ala ser
 2281/761 2311/771
 CTT GCA GCA CTG CGC CTG GCC AGC CCC GAA CCC CTT GTG GCC TTC TCC CAC CAC GTG CTG

leu ala ala leu arg leu ala ser pro glu	pro leu val ala phe ser his his val leu
2341/781	2371/791
GAC AAG CTC GTG CGT CTG GTC ATC AGG CCC	CCG ATC ATC AGT GGC CAG ATT GTG AAC CTG
asp lys leu val arg leu val ile arg pro	pro ile ile ser gly gln ile val asn leu
2401/801	2431/811
GGC CGT GGA GCC TTT GAA GCA ATG GCC CAT	GTA GTC AGC CTT GTT CAC CGG AGC CTG GAG
gly arg gly ala phe glu ala met ala his	val val ser leu val his arg ser leu glu
2461/821	2491/831
GCA GCC CAG GAT GCC CGC GGT CAC TGC CCA	CAG CTG GCT GCC TAC GTC CAC TAC GCC TTT
ala ala gln asp ala arg gly his cys pro	gln leu ala ala tyr val his tyr ala phe
2521/841	2551/851
CGC CTT CCT GGC ACT GAG CCC AGC CTC CCG	GAT GGG GCC CCT CCA GTG ACA GTG CAG GCT
arg leu pro gly thr glu pro ser leu pro	asp gly ala pro pro val thr val gln ala
2581/861	2611/871
GCC ACA CTG GCC CGT GGC TCT GGT CGC CCC	GCA AGC CTC TAC CTG GCG CGT TCC AAG AGC
ala thr leu ala arg gly ser gly arg pro	ala ser leu tyr leu ala arg ser lys ser
2641/881	2671/891
ATC AGC AGC AGC AAC CCT GAC CTC GCC GTG	GCC CCT GGC TCT GTG GAT GAC GAG GTT TCC
ile ser ser ser asn pro asp leu ala val	ala pro gly ser val asp asp glu val ser
2701/901	2731/911
CGC ATC CTG GCC AGC AAG CTG CTT CAC GAG	GAG CTG GCT CTG CAG TGG GTG GTC AGC AGC
arg ile leu ala ser lys leu leu his glu	glu leu ala leu gln trp val val ser ser
2761/921	2791/931
AGT GCC GTA CGC GAG GCC ATC CTC CAG CAC	GCC TGG TTC TTC TTC CAG CTC ATG GTG AAG
ser ala val arg glu ala ile leu gln his	ala trp phe phe phe gln leu met val lys
2821/941	2851/951
AGT ATG GCG CTG CAC CTG CTG CTT GGC CAG	CGA CTA GAC ACA CCC CGC AAG CTG CGC TTC
ser met ala leu his leu leu leu gly gln	arg leu asp thr pro arg lys leu arg phe
2881/961	2911/971
CCC GGA CGC TTC CTG GAC GAC ATC ACT GCC	TTG GTG GGC TCT GTG GGC CTG GAG GTC ATC
pro gly arg phe leu asp asp ile thr ala	leu val gly ser val gly leu glu val ile
2941/981	2971/991
ACC CGT GTC CAC AAG GAT GTG GAG CTG GCC	GAG CAC CTC AAC GCC AGC CTG GCT TTC TTC
thr arg val his lys asp val glu leu ala	glu his leu asn ala ser leu ala phe phe
3001/1001	3031/1011
CTC AGT GAC CTT CTG TCC CTG GTG GAC CGG	GGC TTT GTC TTC AGC CTG GTC CGG GCC CAC
leu ser asp leu leu ser leu val asp arg	gly phe val phe ser leu val arg ala his
3061/1021	3091/1031
TAC AAG CAG GTG GCC ACG CGG CTC CAG TCG	TCC CCT AAT CCA GCA GCC CTG CTG ACC CTG
tyr lys gln val ala thr arg leu gln ser	ser pro asn pro ala ala leu leu thr leu
3121/1041	3151/1051
CGC ATG GAA TTC ACC CGC ATC CTG TGC AGC	CAC GAG CAC TAC GTG ACC CTC AAC CTC CCC
arg met glu phe thr arg ile leu cys ser	his glu his tyr val thr leu asn leu pro
3181/1061	3211/1071
TGC TGC CCC CTG TCA CCT CCA GCC TCG CCC	TCC CCC TCT GTG TCC TCC ACC ACC TCC CAG
cys cys pro leu ser pro pro ala ser pro	ser pro ser val ser ser thr thr ser gln
3241/1081	3271/1091
AGC TCC ACC TTC TCC AGC CAA GCC CCG GAC	CCC AAG GTG ACC AGC ATG TTC GAA CTG AGT
ser ser thr phe ser ser gln ala pro asp	pro lys val thr ser met phe glu leu ser
3301/1101	3331/1111
GGA CCA TTC CGG CAG CAG CAC TTC CTA GCT	GGG CTC CTG CTG ACG GAG CTG GCA CTG GCC
gly pro phe arg gln gln his phe leu ala	gly leu leu leu thr glu leu ala leu ala
3361/1121	3391/1131
CTC GAA CCT GAG GCT GAA GGG GCA TTC CTG	TTG CAC AAG AAG GCC ATC AGT GCT GTG CAC
leu glu pro glu ala glu gly ala phe leu	leu his lys lys ala ile ser ala val his
3421/1141	3451/1151
AGC CTG CTA TGT GGC CAT GAC ACT GAC CCC	CGC TAC GCC GAG GCC ACT GTG AAG GCT CGT
ser leu leu cys gly his asp thr asp pro	arg tyr ala glu ala thr val lys ala arg
3481/1161	3511/1171
GTG GCC GAG CTG TAC CTG CCA CTG CTT TCG	ATT GCA CGG GAT ACC TTG CCA CGG CTG CAT
val ala glu leu tyr leu pro leu leu ser	ile ala arg asp thr leu pro arg leu his

3541/1181	3571/1191
GAC TTT GCT GAG GGC CCA GGT CAG CGG TCA	AGA CTG GCC TCA ATG CTT GAC TCA GAC ACA
asp phe ala glu gly pro gly gln arg ser	arg leu ala ser met leu asp ser asp thr
3601/1201	3631/1211
GAA GGC GAA GGG GAC ATT GCG GGT ACC ATC	AAC CCC TCT GTG GCC ATG GCC ATT GCT GGT
glu gly glu gly asp ile ala gly thr ile	asn pro ser val ala met ala ile ala gly
3661/1221	3691/1231
GGC CCC CTA GCC CCT GGC TCC CGG GCC AGC	ATC TCC CAG GGG CCA CCA ACG GCT TCT CGC
gly pro leu ala pro gly ser arg ala ser	ile ser gln gly pro pro thr ala ser arg
3721/1241	3751/1251
GCA GGC TGT GCC CTC TCT GCT GAG TCA AGC	CGG ACC TTG CTG GCG TGT GTG CTG TGG GTG
ala gly cys ala leu ser ala glu ser ser	arg thr leu leu ala cys val leu trp val
3781/1261	3811/1271
CTG AAA AAC ACC GAG CCG GCG CTC CTG CAG	CGC TGG GCC ACT GAC CTG ACA CTC CCC CAG
leu lys asn thr glu pro ala leu leu gln	arg trp ala thr asp leu thr leu pro gln
3841/1281	3871/1291
CTG GGA CGT CTG TTG GAC TTG CTG TAC CTT	TGC CTG GCT GCC TTT GAG TAC AAG GGG AAA
leu gly arg leu leu asp leu leu tyr leu	cys leu ala ala phe glu tyr lys gly lys
3901/1301	3931/1311
AAG GCC TTT GAA CGC ATC AAC AGC CTC ACA	TTC AAA AAA TCT CTG GAT ATG AAG GCG CGG
lys ala phe glu arg ile asn ser leu thr	phe lys lys ser leu asp met lys ala arg
3961/1321	3991/1331
CTA GAG GAA GCC ATT CTG GGT ACC ATC GGA	GCT CGA CAA GAA ATG GTT CGG CGA AGT CGT
leu glu glu ala ile leu gly thr ile gly	ala arg gln glu met val arg arg ser arg
4021/1341	4051/1351
GAG AGG AGC CCG TTT GGG AAT CCA GAG AAC	GTG CGC TGG CGG AAG AGC GTC ACA CAC TGG
glu arg ser pro phe gly asn pro glu asn	val arg trp arg lys ser val thr his trp
4081/1361	4111/1371
AAG CAA ACC TCA GAC CGC GTG GAC AAG ACC	AAG GAT GAA ATG GAA CAC GAG GCC TTG GTG
lys gln thr ser asp arg val asp lys thr	lys asp glu met glu his glu ala leu val
4141/1381	4171/1391
GAA GGG AAC CTG GCA ACC GAG GCA AGC CTA	GTG GTT CTG GAC ACA CTG GAG ATC ATC GTG
glu gly asn leu ala thr glu ala ser leu	val val leu asp thr leu glu ile ile val
4201/1401	4231/1411
CAG ACG GTG ATG CTT TCA GAA GCC CGG GAG	AGC GTC TTG GGG GCA GTG CTG AAG GTT GTG
gln thr val met leu ser glu ala arg glu	ser val leu gly ala val leu lys val val
4261/1421	4291/1431
CTG TAC AGC CTG GGC AGT GCC CAG AGT GCC	CTC TTC TTG CAG CAT GGC CTG GCC ACC CAG
leu tyr ser leu gly ser ala gln ser ala	leu phe leu gln his gly leu ala thr gln
4321/1441	4351/1451
AGG GCC CTT GTG TCC AAG TTC CCG GAG CTG	CTG TTC GAG GAG GAC ACG GAG CTG TGT GCC
arg ala leu val ser lys phe pro glu leu	leu phe glu glu asp thr glu leu cys ala
4381/1461	4411/1471
GAC CTG TGC CTG AGG CTC CTA CGA CAC TGT	GGC AGC CGC ATC AGC ACC ATC CGC ACG CAC
asp leu cys leu arg leu leu arg his cys	gly ser arg ile ser thr ile arg thr his
4441/1481	4471/1491
GCC AGC GCC TCG CTG TAC CTG CTC ATG CGA	CAG AAC TTC GAG ATC GGC CAC AAC TTT GCC
ala ser ala ser leu tyr leu leu met arg	gln asn phe glu ile gly his asn phe ala
4501/1501	4531/1511
CGT GTG AAG ATG CAG GTC ACC ATG TCT CTC	TCG TCC CTG GTG GGG ACG ACG CAG AAC TTC
arg val lys met gln val thr met ser leu	ser ser leu val gly thr thr gln asn phe
4561/1521	4591/1531
AGT GAA GAG CAC CTG CGA CGT TCA CTC AAA	ACC ATC CTC ACC TAT GCT GAG GAG GAC ATG
ser glu glu his leu arg arg ser leu lys	thr ile leu thr tyr ala glu glu asp met
4621/1541	4651/1551
GGG CTG CGG GAC AGC ACC TTC GCA GAG CAG	GTC CAG GAC CTG ATG TTC AAC CTG CAC ATG
gly leu arg asp ser thr phe ala glu gln	val gln asp leu met phe asn leu his met
4681/1561	4711/1571
ATC CTG ACG GAC ACG GTG AAG ATG AAG GAA	CAC CAG GAG GAC CCT GAG ATG CTC ATC GAC
ile leu thr asp thr val lys met lys glu	his gln glu asp pro glu met leu ile asp
4741/1581	4771/1591

CTC ATG TAC AGA ATT GCC CGG GGC TAC CAG GGC TCA CCG GAC CTT CGG CTG ACC TGG TTG
 leu met tyr arg ile ala arg gly tyr gln gly ser pro asp leu arg leu thr trp leu
 4801/1601 4831/1611
 CAG AAC ATG GCC GGG AAG CAC GCG GAG CTG GGC AAC CAC GCC GAG GCC GCC CAG TGC ATG
 gln asn met ala gly lys his ala glu leu gly asn his ala glu ala ala gln cys met
 4861/1621 4891/1631
 GTG CAC GCG GCC GCC CTC GTG GCT GAG TAC CTC GCC CTG CTC GAG GAC CAG CGC CAC CTG
 val his ala ala ala leu val ala glu tyr leu ala leu leu glu asp gln arg his leu
 4921/1641 4951/1651
 CCC GTG GGC TGC GTT TCC TTC CAG AAC ATC TCA TCC AAC GTG CTA GAG GAG TCC GCC ATC
 pro val gly cys val ser phe gln asn ile ser ser asn val leu glu glu ser ala ile
 4981/1661 5011/1671
 TCC GAC GAC ATC CTG TCG CCC GAC GAG GAG GGC TTC TGC TCC GGG AAG CAC TTC ACT GAG
 ser asp asp ile leu ser pro asp glu glu gly phe cys ser gly lys his phe thr glu
 5041/1681 5071/1691
 CTG GGG CTG GTA GGG TTG CTG GAA CAG GCA GCC GGC TAC TTC ACC ATG GGC GGG CTC TAC
 leu gly leu val gly leu leu glu gln ala ala gly tyr phe thr met gly gly leu tyr
 5101/1701 5131/1711
 GAG GCG GTG AAT GAG GTC TAC AAG AAC CTC ATC CCC ATC CTG GAA GCC CAC CGT GAC TAC
 glu ala val asn glu val tyr lys asn leu ile pro ile leu glu ala his arg asp tyr
 5161/1721 5191/1731
 AAG AAG CTG GCC GCG GTG CAC GGC AAA CTG CAG GAG GCC TTC ACC AAG ATC ATG CAC CAG
 lys lys leu ala ala val his gly lys leu gln glu ala phe thr lys ile met his gln
 5221/1741 5251/1751
 AGT TCC GGC TGG GAG CGC GTG TTC GGG ACG TAT TTC CGC GTG GGC TTC TAC GGC GCC CAC
 ser ser gly trp glu arg val phe gly thr tyr phe arg val gly phe tyr gly ala his
 5281/1761 5311/1771
 TTC GGT GAC CTG GAT GAG CAG GAG TTT GTG TAC AAG GAG CCA TCG ATC ACG AAG CTG GCA
 phe gly asp leu asp glu gln glu phe val tyr lys glu pro ser ile thr lys leu ala
 5341/1781 5371/1791
 GAG ATC TCA CAC CGG CTG GAG GAG TTC TAC ACG GAG AGA TTT GGC GAC GAC GTC GTT GAG
 glu ile ser his arg leu glu glu phe tyr thr glu arg phe gly asp asp val val glu
 5401/1801 5431/1811
 ATT ATC AAA GAC TCT TAC CCT GTG GAC AAG TCC AAG CTT GAC TCA CAA AAG GCC TAC ATC
 ile ile lys asp ser tyr pro val asp lys ser lys leu asp ser gln lys ala tyr ile
 5461/1821 5491/1831
 CAG ATC ACG TAT GTG GAA CCG TAC TTT GAT ACC TAC GAG CTC AAG GAC CGG GTG ACC TAC
 gln ile thr tyr val glu pro tyr phe asp thr tyr glu leu lys asp arg val thr tyr
 5521/1841 5551/1851
 TTT GAC CGC AAC TAT GGG CTT CGC ACA TTC CTG TTC TGC ACG CCG TTC ACG CCG GAT GGG
 phe asp arg asn tyr gly leu arg thr phe leu phe cys thr pro phe thr pro asp gly
 5581/1861 5611/1871
 CGC GCA CAC GGG GAG CTG CCC GAG CAA CAC AAG CGT AAG ACG CTG CTC AGC ACC GAC CAC
 arg ala his gly glu leu pro glu gln his lys arg lys thr leu leu ser thr asp his
 5641/1881 5671/1891
 GCC TTC CCC TAC ATC AAG ACT CGC ATC CGT GTG TGC CAC CGG GAG GAG ACG GTG CTG ACG
 ala phe pro tyr ile lys thr arg ile arg val cys his arg glu glu thr val leu thr
 5701/1901 5731/1911
 CCA GTG GAG GTG GCC ATC GAG GAC ATG CAG AAG AAG ACA CGG GAG CTG GCC TTT GCC ACC
 pro val glu val ala ile glu asp met gln lys lys thr arg glu leu ala phe ala thr
 5761/1921 5791/1931
 GAG CAG GAC CCA CCA GAT GCT AAG ATG CTA CAG ATG GTG CTT CAG GGC TCT GTA GGG CCC
 glu gln asp pro pro asp ala lys met leu gln met val leu gln gly ser val gly pro
 5821/1941 5851/1951
 ACC GTG AAC CAG GGT CCC CTG GAG GTG GCC CAG GTG TTT TTA GCA GAG ATC CCG GAA GAC
 thr val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro glu asp.
 5881/1961 5911/1971
 CCC AAG CTC TTC CGG CAT CAC AAC AAA TTG CGG CTC TGC TTC AAG GAC TTC TGC AAG AAA
 pro lys leu phe arg his his asn lys leu arg leu cys phe lys asp phe cys lys lys
 5941/1981 5971/1991
 TGT GAG GAT GCG CTG CGG AAA AAT AAG GCC CTG ATT GGG CCG GAC CAG AAG GAG TAC CAC

cys glu asp ala leu arg lys asn lys ala leu ile gly pro asp gln lys glu tyr his
6001/2001 6031/2011
CGT GAG CTG GAG CGC AAC TAC TGC CGC CTG CGG GAG GCT CTG CAG CCC CTG CTT ACC CAG
arg glu leu glu arg asn tyr cys arg leu arg glu ala leu gln pro leu leu thr gln
6061/2021 6091/2031
CGC CTG CCC CAG CTG ATG GCA CCC ACC CCA CCC GGC CTC AGG AAC TCC TTG AAC AGA GCA
arg leu pro gln leu met ala pro thr pro pro gly leu arg asn ser leu asn arg ala
6121/2041 6151/2051
AGT TTC CGA AAG GCA GAC CTC TGA GCC CAC AAG GAC CAA AGC TGT ACC TAG AGG AAC CAG
ser phe arg lys ala asp leu OPA
6181/2061 6211/2071
CAC CCG GGC CTC AGC TGT CTG TGC TGC GAG GGG AGT CTG CCC TGG TGC CCA CTG GGC TGT
6241/2081 6271/2091
GGG GTG ACC ACA CTG TAC TTG GGG CTG GGC CCT CTG CCC CTG TGT CCC CAT CTG TGT GCA
6301/2101 6331/2111
CTG ATG CTT CCT CCC TTT TTT AAT TTA AAA TGG TTT TTA TAA GCA AAA AAA AAA AAA AAA

-111

CGGTAACCGCCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAAGTGTGAATCTTTCAAAGCCTCAGTTTTATGACC
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1	31/11
ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG	CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT
Met thr his leu asn ser leu asp val gln	leu ala gln glu leu gly asp phe thr asp
61/21	91/31
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG	GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG
asp asp leu asp val val phe thr pro lys	glu cys arg thr leu gln pro ser leu pro
121/41	151/51
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC	AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG
glu glu gly val glu leu asp pro his val	arg asp cys val gln thr tyr ile arg glu
181/61	211/71
TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA	AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT
trp leu ile val asn arg lys asn gln gly	ser pro glu ile cys gly phe lys lys thr
241/81	271/91
GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT	CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG
gly ser arg lys asp phe his lys thr leu	pro lys gln thr phe glu ser glu thr leu
301/101	331/111
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC	CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG
glu cys ser glu pro ala ala gln ala gly	pro arg his leu asn val leu cys asp val
361/121	391/131
TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC	TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG
ser gly lys gly pro val thr ala cys asp	phe asp leu arg ser leu gln pro asp lys
421/141	451/151
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT	GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG
arg leu glu asn leu leu gln gln val ser	ala glu asp phe glu lys gln asn glu glu
481/161	511/171
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC	TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG
ala arg arg thr asn arg gln ala glu leu	phe ala leu tyr pro ser val asp glu glu
541/181	571/191
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA	TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA
asp ala val glu ile arg pro val pro glu	cys pro lys glu his leu gly asn arg ile
601/201	631/211
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG	ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT
leu val lys leu leu thr leu lys phe glu	ile glu ile glu pro leu phe ala ser ile
661/221	691/231
GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG	ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC
ala leu tyr asp val lys glu arg lys lys	ile ser glu asn phe his cys asp leu asn
721/241	751/251
TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT	CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG
ser asp gln phe lys gly phe leu arg ala	his thr pro ser val ala ala ser ser gln
781/261	811/271
GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC	CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG
ala arg ser ala val phe ser val thr tyr	pro ser ser asp ile tyr leu val val lys
841/281	871/291
ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT	GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC
ile glu lys val leu gln gln gly asp ile	gly asp cys ala glu pro tyr thr val ile
901/301	931/311
AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA	AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA
lys glu ser asp gly gly lys ser lys glu	lys ile glu lys leu lys leu gln ala glu
961/321	991/331
TCC TTC TGC CAG CGT TTG GGG AAA TAC CGG	ATG CCC TTT GCC TGG GCA CCC ATA AGC TTA
ser phe cys gln arg leu gly lys tyr arg	met pro phe ala trp ala pro ile ser leu

1021/341	TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG	1051/351	AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT
1081/361	ser ser phe phe asn val ser thr leu glu	1111/371	arg glu val thr asp val asp ser val val
1141/381	GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA	1171/391	TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA
1201/401	gly arg ser pro val gly glu arg arg thr	1231/411	leu ala gln ser arg arg leu ser glu arg
1261/421	GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA	1291/431	TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT
1321/441	ala leu ser leu glu glu asn gly val gly	1351/451	ser asn phe lys thr ser thr leu ser val
1381/461	AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC	1411/471	CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA
1441/481	ser ser phe phe lys gln glu gly asp arg	1471/491	leu ser asp glu asp leu phe lys phe leu
1501/501	GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG	1531/511	AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA
1561/521	ala asp tyr lys arg ser ser ser leu gln	1591/531	arg arg val lys ser ile pro gly leu leu
1621/541	AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC	1651/551	ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG
1681/561	arg leu glu ile ser thr ala pro glu ile	1711/571	ile asn cys cys leu thr pro glu met leu
1741/581	CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA	1771/591	CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
1801/601	pro val lys pro phe pro glu asn arg thr	1831/611	arg pro his lys glu ile leu glu phe pro
1861/621	ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG	1891/631	TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG
1921/641	thr arg glu val tyr val pro his thr val	1951/651	tyr arg asn leu leu tyr val tyr pro gln
1981/661	AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA	2011/671	GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT
2041/681	arg leu asn phe val asn lys leu ala ser	2071/691	ala arg asn ile thr ile lys ile gln phe
2101/701	ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG	2131/711	CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
	met cys gly glu asp ala ser asn ala met		pro val ile phe gly lys ser ser gly pro
	GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT		ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT
	glu phe leu gln glu val tyr thr ala val		thr tyr his asn lys ser pro asp phe tyr
	GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG		CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC
	glu glu val lys ile lys leu pro ala lys		leu thr val asn his his leu leu phe thr
	TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA		GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT
	phe tyr his ile ser cys gln gln lys gln		gly ala ser val glu thr leu leu gly tyr
	TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT		CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT
	ser trp leu pro ile leu leu asn glu arg		leu gln thr gly ser tyr cys leu pro val
	GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC		ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG
	ala leu glu lys leu pro pro asn tyr ser		met his ser ala glu lys val pro leu gln
	AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT		AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT
	asn pro pro ile lys trp ala glu gly his		lys gly val phe asn ile glu val gln ala
	GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC		CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC
	val ser ser val his thr gln asp asn his		leu glu lys phe phe thr leu cys his ser
	CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC		GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG
	leu glu ser gln val thr phe pro ile arg		val leu asp gln lys ile ser glu met ala
	CTG GAG CAT GAG CTG AAG CTC AGC ATC ATC		TGC CTG AAC TCC TCC CGC CTG GAG CCG CTC
	leu glu his glu leu lys leu ser ile ile		cys leu asn ser ser arg leu glu pro leu

2161/721	GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG	2191/731	CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
val leu phe leu his leu val leu asp lys	leu phe gln leu ser val gln pro met val		
2221/741	ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG	2251/751	TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
ile ala gly gln thr ala asn phe ser gln	phe ala phe glu ser val val ala ile ala		
2281/761	AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC	2311/771	AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
asn ser leu his asn ser lys asp leu ser	lys asp gln his gly arg asn cys leu leu		
2341/781	GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG	2371/791	CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
ala ser tyr val his tyr val phe arg leu	pro glu val gln arg asp val pro lys ser		
2401/801	GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG	2431/811	AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
gly ala pro thr ala leu leu asp pro arg	ser tyr his thr tyr gly arg thr ser ala		
2461/821	GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC	2491/831	CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
ala ala val ser ser lys leu leu gln ala	arg val met ser ser ser asn pro asp leu		
2521/841	GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA	2551/851	GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
ala gly thr his ser ala ala asp glu glu	val lys asn ile met ser ser lys ile ala		
2581/861	GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT	2611/871	TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
asp arg asn cys ser arg met ser tyr tyr	cys ser gly ser ser asp ala pro ser ser		
2641/881	CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG	2671/891	CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
pro ala ala pro arg pro ala ser lys lys	his phe his glu glu leu ala leu gln met		
2701/901	GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG	2731/911	GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
val val ser thr gly met val lys ser met	ala gln his val his asn met asp lys arg		
2761/921	GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC	2791/931	CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
asp ser phe arg arg thr arg phe ser asp	arg phe met asp asp ile thr thr ile val		
2821/941	AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT	2851/951	TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
asn val val thr ser glu ile ala ala leu	leu val lys pro gln lys glu asn glu gln		
2881/961	GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC	2911/971	TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
ala glu lys met asn ile ser leu ala phe	phe leu tyr asp leu leu ser leu met asp		
2941/981	CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT	2971/991	TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
arg gly phe val phe asn leu ile arg his	tyr cys ser gln leu ser ala lys leu ser		
3001/1001	AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA	3031/1011	GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
asn leu pro thr leu ile ser met arg leu	glu phe leu arg ile leu cys ser his glu		
3061/1021	CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG	3091/1031	AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
his tyr leu asn leu asn leu phe phe met	asn ala asp thr ala pro thr ser pro cys		
3121/1041	CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC	3151/1051	TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
pro ser ile ser ser gln asn ser ser ser	cys ser ser phe gln asp gln lys ile ala		
3181/1061	AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC	3211/1071	CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
ser met phe asp leu thr ser glu tyr arg	gln gln his phe leu thr gly leu leu phe		
3241/1081	ACA GAA CTG GCT GCT GCC CTG GAT GCC GAA	3271/1091	GGG GAA GGA ATC AGC AAA GTA CAA AGG AAA
thr glu leu ala ala ala leu asp ala glu	gly glu gly ile ser lys val gln arg lys		

3301/1101	GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT	3331/1111	TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
3361/1121	ala val ser ala ile his ser leu leu ser	3391/1131	ser his asp leu asp pro arg cys val lys
3421/1141	CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT	3451/1151	TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
3481/1161	pro glu val lys val lys ile ala ala leu	3511/1171	tyr leu pro leu val gly ile ile leu asp
3541/1181	GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT	3571/1191	GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
3601/1201	ala leu pro gln leu cys asp phe thr val	3631/1211	ala asp thr arg arg tyr arg thr ser gly
3661/1221	TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC	3691/1231	ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
3721/1241	ser asp glu glu gln glu gly ala gly ala	3751/1251	ile asn gln asn val ala leu ala ile ala
3781/1261	GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA	3811/1271	ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
3841/1281	gly asn asn phe asn leu lys thr ser gly	3871/1291	ile val leu ser ser leu pro tyr lys gln
3901/1301	TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC	3931/1311	AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
3961/1321	tyr asn met leu asn ala asp thr thr arg	3991/1331	asn leu met ile cys phe leu trp ile met
4021/1341	AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG	4051/1351	TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
4081/1361	lys asn ala asp gln ser leu ile arg lys	4111/1371	trp ile ala asp leu pro ser thr gln leu
4141/1381	AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT	4171/1391	GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
4201/1401	asn arg ile leu asp leu leu phe ile cys	4231/1411	val leu cys phe glu tyr lys gly lys gln
4261/1421	AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG	4291/1431	CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
4321/1441	ser ser asp lys val ser thr gln val leu	4351/1451	gln lys ser arg asp val lys ala arg leu
4381/1461	GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC	4411/1471	AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA
	glu glu ala leu leu arg gly glu gly ala		arg gly glu met met arg arg arg ala pro
	GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA		AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
	gly asn asp arg phe pro gly leu asn glu		asn leu arg trp lys lys glu gln thr his
	TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA		ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
	trp arg gln ala asn glu lys leu asp lys		thr lys ala glu leu asp gln glu ala leu
	ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT		TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
	ile ser gly asn leu ala thr glu ala his		leu ile ile leu asp met gln glu asn ile
	ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA		GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
	ile gln ala ser ser ala leu asp cys lys		asp ser leu leu gly gly val leu arg val
	CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT		ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA
	leu val asn ser leu asn cys asp gln ser		thr thr tyr leu thr his cys phe ala thr
	CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC		TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT
	leu arg ala leu ile ala lys phe gly asp		leu leu phe glu glu glu val glu gln cys
	TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC		TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
	phe asp leu cys his gln val leu his his		cys ser ser ser met asp val thr arg ser
	CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG		AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT
	gln ala cys ala thr leu tyr leu leu met		arg phe ser phe gly ala thr ser asn phe
	GCA AGA GTA AAG ATG CAA GTA ACC ATG TCC		CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC
	ala arg val lys met gln val thr met ser		leu ala ser leu val gly arg ala pro asp

4441/1481	TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG	4471/1491	AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
phe asn glu glu his leu arg arg ser leu	arg thr ile leu ala tyr ser glu glu asp		
4501/1501	ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC	4531/1511	CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT
thr ala met gln met thr pro phe pro thr	gln val glu glu leu leu cys asn leu asn		
4561/1521	AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG	4591/1531	GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG
ser ile leu tyr asp thr val lys met arg	glu phe gln glu asp pro glu met leu met		
4621/1541	GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC	4651/1551	CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG
asp leu met tyr arg ile ala lys ser tyr	gln ala ser pro asp leu arg leu thr trp		
4681/1561	CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG	4711/1571	AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC
leu gln asn met ala glu lys his thr lys	lys lys cys tyr thr glu ala ala met cys		
4741/1581	CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG	4771/1591	TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC
leu val his ala ala ala leu val ala glu	tyr leu ser met leu glu asp his ser tyr		
4801/1601	CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT	4831/1611	ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG
leu pro val gly ser val ser phe gln asn	ile ser ser asn val leu glu glu ser val		
4861/1621	GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG	4891/1631	GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC
val ser glu asp thr leu ser pro asp glu	asp gly val cys ala gly gln tyr phe thr		
4921/1641	GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG	4951/1651	GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA
glu ser gly leu val gly leu leu glu gln	ala ala glu leu phe ser thr gly gly leu		
4981/1661	TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG	5011/1671	GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA
tyr glu thr val asn glu val tyr lys leu	val ile pro ile leu glu ala his arg glu		
5041/1681	TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG	5071/1691	CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC
phe arg lys leu thr leu thr his ser lys	leu gln arg ala phe asp ser ile val asn		
5101/1701	AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC	5131/1711	TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT
lys asp his lys arg met phe gly thr tyr	phe arg val gly phe phe gly ser lys phe		
5161/1721	GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC	5191/1731	AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG
gly asp leu asp glu gln glu phe val tyr	lys glu pro ala ile thr lys leu pro glu		
5221/1741	ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT	5251/1751	CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG
ile ser his arg leu glu ala phe tyr gly	gln cys phe gly ala glu phe val glu val		
5281/1761	ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC	5311/1771	AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG
ile lys asp ser thr pro val asp lys thr	lys leu asp pro asn lys ala tyr ile gln		
5341/1781	ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG	5371/1791	TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT
ile thr phe val glu pro tyr phe asp glu	tyr glu met lys asp arg val thr tyr phe		
5401/1801	GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG	5431/1811	TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG
glu lys asn phe asn leu arg arg phe met	tyr thr thr pro phe thr leu glu gly arg		
5461/1821	CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA	5491/1831	AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC
pro arg gly glu leu his glu gln tyr arg	arg asn thr val leu thr thr met his ala		
5521/1841	TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC	5551/1851	ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG
phe pro tyr ile lys thr arg ile ser val	ile gln lys glu glu phe val leu thr pro		

5581/1861	5611/1871
ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG	AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
ile glu val ala ile glu asp met lys lys	lys thr leu gln leu ala val ala ile asn
5641/1881	5671/1891
CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG	ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
gln glu pro pro asp ala lys met leu gln	met val leu gln gly ser val gly ala thr
5701/1901	5731/1911
GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA	GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
val asn gln gly pro leu glu val ala gln	val phe leu ala glu ile pro ala asp pro
5761/1921	5791/1931
AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG	TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
lys leu tyr arg his his asn lys leu arg	leu cys phe lys glu phe ile met arg cys
5821/1941	5851/1951
GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC	ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
gly glu ala val glu lys asn lys arg leu	ile thr ala asp gln arg glu tyr gln gln
5881/1961	5911/1971
GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA	GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
glu leu lys lys asn tyr asn lys leu lys	glu asn leu arg pro met ile glu arg lys
5941/1981	5971/1991
ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA	GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
ile pro glu leu tyr lys pro ile phe arg	val glu ser gln lys arg asp ser phe his
6001/2001	6031/2011
AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG	TTG TCA CAG GGC AGC TAA
arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH	

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAATGGGACATT
TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
TTATTAAAGTGTTGTTTTCCACAATGTACCAAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
TGAGAGATGATTTCTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAATGGAAAAATTATCC
ACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACCTGTAGGAGTACGAAACATTTTCAATAAAT
CTACAAAGGGAAGCCTTACTACAATTCCAAAAATCATCATGGTTGGAAATTTGGGAGGAGATTATTTGTGAACCTTGTTAC
CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
TAGAAGAATACATTCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAAATCACAGATACTGCTTT
CACTTAAATGGAAACAATTCTCCGATAATGCTTTGCTTTTTTCTTATGTCACTCTTGTTACTATCTATTTTTCTCCTC
TCTGGGACCAAGTTTCTTTTTATAAAGCAATAATATCTCTGTTTTTCATTTCAGAACATTGTGCTGTCTGTCAGCATATGT
ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
AGAATTAAATTATATATTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAATTGCAAGCTAAAAAA
AAAAAAAAAAAACTCG

Exon 1A (- 216 to -95, 'P2')

CCCATTAGGAGGTCTACCCACCCTGATTGGAGGACATGGGGCTGGAGGCTGAAGATGGAGACCAGATCACAAGGGATCTAATAAG
CCTTGCTGAACAGTTTGAGCTTTATTCTACAGACTCT -95

Exon 1B (-381 to -95, 'GR3.3')

AAATTTTAGTTGGAGAATGCACAGGAGAAGGTGTAGACATAGTTTTGTCTGTGTGTCAGACACCTTGATAGCAAACACTATAGGTAG
AGGCTTCTGGAGGCAGGATTGCTCTTAGTCTAAGGTCTTATGGTAACATTTGCAGGGGATACGGGTAGCATTACAAAATGGGGA
TGCTTCAGGAAGGGCGTGGGCGAGTGCTTCTTGCTATTACTTCTTGTAAACAAAGCTAGTCTAGGCTTTTGGGTATGTTCAACAC
TGCATGGCCTTTGGAGCACTTTTATGGGAAGA -95

Exon 1C (-415 to -95, 'GR3.4')

AAAGACAGGAACGCACTGCCACATTGAGAGGATAGCATTTTTAGTTGGAGAGTGTACAGGAGAAGGTGTAGACATAGTTTTGTCTG
TGTCAGACACCTNGATAGCAAACACTATAGGTAGAGGCTTCTGGAGGCAGGATTGCTCTTAGTCTAAGGTCTTATGGTAACATTT
GCAGGGGATACGGGTAGCATTACAAAATGGGGATGCTTCAGGAAGGGCGTGGGCGAGTGCTTCTTGCTATTACTTCTTGTAAAC
AAAGCTAGTCTAGGCTTTTGGGTATGTTCAACACTGCATGGCCTTTGGAGCACTTTTATGGGAAGA -95

Exon 1D (-186 to -95, 'GR8.2')

AATTAGAAACAACGGGGTTCTGCGACAGAGTGGGCGCAGGGTCATCCACCGCAGGGAGAGTGTGTCCCTCGGGGACACGCGAGCG
CTCCAGA -95

Exon 1E (-217 to -95, 'GR8.3')

AAGTTGAAGGGGTGCTGCTGCGGAGGAAGGGCATTAGAAACAACGGGGTTCTGCGACAGAGTGGGCGCAGGGTCATCCACCGCAG
GGAGAGTGTGTCCCTCGGGGACACGCGAGCGCTCCAGA -95

Exon 1F (-166 to -95, 'GR8.4')

AAACCAAAGCTAGTCTAGGCTTCTTGGGTATGTTCAACACTGCATGGCCTTTGGAGCACTTATATGGGAAGA -95

Exon 1G (-250 to -95, EST 850011)

GTCCACCCGCCCCGCGAGGTCCGCCCCCGCCGAGACCCGCCCCGCGCGCTGCCATGGCCGAAGTGCGCAAATTCACCAAACG
GCTCAGCAAGCCTGGCAGCGCGGCTGANATCCGGCAGACGTGTCTGAGGCCGTGCGGGGCTCCGTGGTGCT -95

Exon 1H (-187 to -95, 'GR1988')

AAATTAGAAACAACGGGGTTCTGCGACAGAGTGGGCGCAGGGTCATCCACCGCAGGGAGAGTGTGTCCCTCGGGGACACGCGAGC
GCTCCAGA -95

Exon 1I (-144 to -95, 'GR2005')

AACTCCCGGATGCGGCTGCACCAGCAACATCAGCTGCGGGGAGCCCGAGC -95

Exon 1J (-131 to -95, 'GR1986')

AACCCAGAAAGCCCCGGGCGCCCAAGCTCGGGCTGGC -95

-94

G GAA AAG GCC AAA GTT GTT GAG CCC CTG GAC TAT GAG AAT GTT ATT GCC CAA AGA AAA -37

ACC CAG ATT TAC AGC GAC CCC CTC CGA GAT CTG CTT ¹ ATG TTC CCA ATG GAA GAT ATA TCT 24
met phe pro met glu asp ile ser

ATC TCG GTG ATA GGT CGT CAG CGC AGA ACG GTG CAG TCT ACT GTA CCA GAA GAT GCT GAA 84
ile ser val ile gly arg gln arg arg thr val gln ser thr val pro glu asp ala glu

AAG AGG GCC CAG AGT TTA TTT GTT AAA GAG TGT ATT AAA ACC TAT AGC ACA GAT TGG CAC 144
lys arg ala gln ser leu phe val lys glu cys ile lys thr tyr ser thr asp trp his.

A

FIG. 8 20
1 of 7

GTG GTA AAC TAC AAG TAT GAG GAC TTC TCT GGG GAC TTT CGA ATG TTG CCA TGT AAA TCT 204
 val val asn tyr lys tyr glu asp phe ser gly asp phe arg met leu pro cys lys ser
 TTG AGA CCA GAA AAG ATT CCT AAT CAT GTA TTT GAG ATA GAT GAA GAC TGT GAG AAA GAT 264
 leu arg pro glu lys ile pro asn his val phe glu ile asp glu asp cys glu lys asp
 GAG GAC TCA TCT TCT TTA TGT TCT CAG AAG GGT GGT GTG ATA AAA CAA GGC TGG TTG CAT 324
 glu asp ser ser ser leu cys ser gln lys gly gly val ile lys gln gly trp leu his
 AAA GCA AAT GTA AAT AGT ACC ATC ACA GTA ACC ATG AAG GTA TTC AAG AGA CGA TAT TTT 384
 lys ala asn val asn ser thr ile thr val thr met lys val phe lys arg arg tyr phe
 TAC TTG ACC CAA CTT CCT GAC GGT TCA TAT ATT CTC AAT TCC TAT AAA GAT GAG AAA AAT 444
 tyr leu thr gln leu pro asp gly ser tyr ile leu asn ser tyr lys asp glu lys asn
 TCA AAA GAA TCG AAA GGT TGC ATC TAC TTG GAC GCC TGC ATT GAT GTT GTT CAG TGC CCC 504
 ser lys glu ser lys gly cys ile tyr leu asp ala cys ile asp val val gln cys pro
 AAA ATG CGC CGT CAT GCT TTT GAA CTC AAG ATG TTA GAT AAA TAT AGC CAT TAT CTG GCT 564
 lys met arg arg his ala phe glu leu lys met leu asp lys tyr ser his tyr leu ala
 GCT GAA ACT GAG CAG GAA ATG GAG GAA TGG TTG ATA ACT TTG AAA AAG ATT ATT CAG ATC 624
 ala glu thr glu gln glu met glu glu trp leu ile thr leu lys lys ile ile gln ile
 AAC ACC GAC AGT TTA GTT CAA GAA AAA AAG GAG ACG GTA GAA ACA GCA CAA GAT GAT GAA 684
 asn thr asp ser leu val gln glu lys lys glu thr val glu thr ala gln asp asp glu
 ACT AGC AGC CAA GGA AAA GCC GAG AAC ATC ATG GCA AGT TTG GAA AGG AGC ATG CAT CCG 744
 thr ser ser gln gly lys ala glu asn ile met ala ser leu glu arg ser met his pro
 GAA CTG ATG AAG TAT GGA AGA GAA ACT GAA CAA CTA AAC AAA CTC AGT AGA GGA GAT GGA 804
 glu leu met lys tyr gly arg glu thr glu gln leu asn lys leu ser arg gly asp gly
 AGA CAG AAT CTC TTT TCT TTT GAT TCA GAA GTT CAG AGG TTG GAC TTT TCA GGA ATT GAA 864
 arg gln asn leu phe ser phe asp ser glu val gln arg leu asp phe ser gly ile glu
 CCT GAT ATA AAG CCA TTT GAA GAA AAA TGC AAT AAA CGT TTC CTG GTG AAT TGC CAT GAT 924
 pro asp ile lys pro phe glu glu lys cys asn lys arg phe leu val asn cys his asp
 TTA ACT TTC AAT ATC TTG GGC CAA ATT GGA GAC AAT GCA AAA GGA CCA CCC ACA AAT GTT 984
 leu thr phe asn ile leu gly gln ile gly asp asn ala lys gly pro pro thr asn val
 GAG CCC TTT TTT ATC AAT CTT GCC TTA TTT GAT GTA AAG AAC AAT TGT AAG ATT TCA GCA 1044
 glu pro phe phe ile asn leu ala leu phe asp val lys asn asn cys lys ile ser ala
 GAC TTT CAT GTA GAC CTG AAT CCC CCA TCT GTC CGT GAA ATG CTG TGG GGC TCT TCA ACC 1104
 asp phe his val asp leu asn pro pro ser val arg glu met leu trp gly ser ser thr
 CAA CTG GCC AGT GAC GGT AGC CCA AAG GGC TCT TCA CCC GAA TCT TAC ATT CAT GGA ATT 1164
 gln leu ala ser asp gly ser pro lys gly ser ser pro glu ser tyr ile his gly ile
 GCC GAA TCT CAG TTA CGC TAC ATA CAA CAG GGA ATT TTC TCA GTG ACG AAT CCA CAT CCT 1224
 ala glu ser gln leu arg tyr ile gln gln gly ile phe ser val thr asn pro his pro
 GAA ATT TTT CTA GTT GCC AGA ATT GAA AAG GTA CTA CAG GGA AAC ATT ACA CAC TGT GCA 1284
 glu ile phe leu val ala arg ile glu lys val leu gln gly asn ile thr his cys ala

GAA CCC TAT ATC AAA AAT TCT GAT CCA GTA AAG ACG GCC CAG AAG GTG CAC AGG ACA GCT 1344
 glu pro tyr ile lys asn ser asp pro val lys thr ala gln lys val his arg thr ala
 AAA CAA GTG TGT AGC CGC CTT GGA CAA TAC AGA ATG CCC TTC GCT TGG GCT GCC AGA CCC 1404
 lys gln val cys ser arg leu gly gln tyr arg met pro phe ala trp ala ala arg pro
 ATT TTC AAA GAT ACT CAA GGC TCT CTT GAT CTG GAT GGG AGA TTT TCT CCT CTG TAT AAA 1464
 ile phe lys asp thr gln gly ser leu asp leu asp gly arg phe ser pro leu tyr lys
 CAA GAC AGT AGC AAG CTT TCA AGT GAA GAC ATT CTC AAG TTG CTC TCA GAA TAT AAG AAG 1524
 gln asp ser ser lys leu ser ser glu asp ile leu lys leu leu ser glu tyr lys lys
 CCA GAA AAG ACC AAA CTG CAG ATT ATT CCT GGG CAG CTA AAC ATC ACA GTA GAA TGT GTT 1584
 pro glu lys thr lys leu gln ile ile pro gly gln leu asn ile thr val glu cys val
 CCT GTG GAT TTA TCA AAT TGT ATT ACT TCT TCA TAT GTG CCC TTG AAG CCT TTT GAA AAG 1644
 pro val asp leu ser asn cys ile thr ser ser tyr val pro leu lys pro phe glu lys
 AAT TGC CAA AAT ATT ACT GTG GAG GTT GAA GAG TTT GTT CCA GAA ATG ACA AAA TAT TGT 1704
 asn cys gln asn ile thr val glu val glu glu phe val pro glu met thr lys tyr cys
 TAT CCA TTT ACT ATT TAC AAA AAC CAT CTG TAT GTA TAT CCC CTG CAA TTA AAA TAC GAT 1764
 tyr pro phe thr ile tyr lys asn his leu tyr val tyr pro leu gln leu lys tyr asp
 AGC CAG AAA ACA TTT GCC AAG GCA AGG AAC ATT GCA GTC TGT GTG GAA TTC CGG GAT TCA 1824
 ser gln lys thr phe ala lys ala arg asn ile ala val cys val glu phe arg asp ser
 GAT GAA AGT GAC GCT AGT GCC CTA AAG TGT ATT TAT GGA AAA CCT GCA GGG TCT GTT TTT 1884
 asp glu ser asp ala ser ala leu lys cys ile tyr gly lys pro ala gly ser val phe
 ACC ACA AAT GCT TAT GCT GTT GTC TCG CAT CAC AAC CAA AAT CCA GAG TTC TAT GAT GAG 1944
 thr thr asn ala tyr ala val val ser his his asn gln asn pro glu phe tyr asp glu
 ATT AAA ATT GAG CTT CCC ATT CAC CTA CAT CAA AAA CAT CAT TTG CTT TTC ACT TTT TAT 2004
 ile lys ile glu leu pro ile his leu his gln lys his his leu leu phe thr phe tyr
 CAT GTA AGT TGT GAA ATT AAC ACA AAG GGA ACA ACC AAA AAG CAA GAC ACA GTT GAA ACT 2064
 his val ser cys glu ile asn thr lys gly thr thr lys lys gln asp thr val glu thr
 CCA GTT GGG TTT GCC TGG GTA CCT TTG CTG AAA GAT GGT AGA ATC ATC ACA TTT GAG CAG 2124
 pro val gly phe ala trp val pro leu leu lys asp gly arg ile ile thr phe glu gln
 CAG CTG CCA GTT TCC GCC AAT CTT CCC CCA GGC TAC TTG AAT CTG AAT GAT GCA GAA TCA 2184
 gln leu pro val ser ala asn leu pro pro gly tyr leu asn leu asn asp ala glu ser
 AGA AGG CAA TGT AAC GTG GAT ATT AAA TGG GTA GAT GGT GCA AAG CCT TTG TTG AAG TTT 2244
 arg arg gln cys asn val asp ile lys trp val asp gly ala lys pro leu leu lys phe
 AAA AGC CAC TTA GAA TCT ACC ATT TAC ACT CAA GAT CTG CAT GTG CAC AAA TTC TTC CAT 2304
 lys ser his leu glu ser thr ile tyr thr gln asp leu his val his lys phe phe his
 CAT TGC CAG CTG ATT CAG TCA GGC TCG AAA GAA GTT CCA GGG GAG CTC ATT AAA TAT TTA 2364
 his cys gln leu ile gln ser gly ser lys glu val pro gly glu leu ile lys tyr leu
 AAG TGT TTG CAT GCC ATG GAG ATC CAA GTC ATG ATA CAG TTT CTA CCT GTA ATT CTT ATG 2424
 lys cys leu his ala met glu ile gln val met ile gln phe leu pro val ile leu met
 CAA CTC TTC CGA GTT CTC ACA AAT ATG ACC CAT GAA GAT GAC GTT CCT ATC AAC TGC ACC 2484
 gln leu phe arg val leu thr asn met thr his glu asp asp val pro ile asn cys thr

ATG GTT CTC TTA CAT ATT GTA TCA AAG TGC CAT GAA GAA GGC TTG GAT AGT TAT CTA AGA 2544
 met val leu leu his ile val ser lys cys his glu glu gly leu asp ser tyr leu arg

 TCA TTC ATA AAG TAT AGC TTC CGA CCT GAA AAA CCG AGT GCT CCT CAG GCC CAG CTG ATA 2604
 ser phe ile lys tyr ser phe arg pro glu lys pro s r ala pro gln ala gln leu ile

 CAT GAA ACC CTG GCT ACT ACG ATG ATA GCA ATA TTG AAA CAG TCT GCA GAT TTT TTA TCA 2664
 his glu thr leu ala thr thr met ile ala ile leu lys gln ser ala asp phe leu ser

 ATA AAC AAA TTG CTA AAG TAC TCA TGG TTT TTC TTT GAA ATA ATT GCA AAG TCA ATG GCC 2724
 ile asn lys leu leu lys tyr ser trp phe phe phe glu ile ile ala lys ser met ala

 ACA TAC TTG TTG GAA GAG AAT AAG ATT AAG CTT CCC CGA GGC CAG AGA TTT CCC GAG ACA 2784
 thr tyr leu leu glu glu asn lys ile lys leu pro arg gly gln arg phe pro glu thr

 TAT CAT CAT GTC TTA CAT TCA CTG CTT CTT GCA ATA ATT CCC CAT GTG ACT ATT CGG TAT 2844
 tyr his his val leu his ser leu leu leu ala ile ile pro his val thr ile arg tyr

 GCG GAG ATT CCC GAT GAG TCC AGA AAT GTG AAC TAT AGT TTG GCT AGC TTC CTG AAG CGC 2904
 ala glu ile pro asp glu ser arg asn val asn tyr ser leu ala ser phe leu lys arg

 TGT TTG ACA CTA ATG GAT AGA GGA TTT ATT TTC AAT TTA ATA AAT GAC TAT ATA TCT GGA 2964
 cys leu thr leu met asp arg gly phe ile phe asn leu ile asn asp tyr ile ser gly

 TTC AGC CCC AAA GAT CCT AAG GTT CTG GCT GAA TAC AAG TTT GAA TTT CTG CAA ACA ATT 3024
 phe ser pro lys asp pro lys val leu ala glu tyr lys phe glu phe leu gln thr ile

 TGC AAT CAC GAA CAT TAC ATT CCT CTG AAC TTG CCA ATG GCA TTT GCA AAA CCT AAA CTG 3084
 cys asn his glu his tyr ile pro leu asn leu pro met ala phe ala lys pro lys leu

 CAG CGG GTT CAA GAT TCA AAT CTT GAA TAC AGT TTA TCA GAT GAG TAT TGC AAG CAT CAC 3144
 gln arg val gln asp ser asn leu glu tyr ser leu ser asp glu tyr cys lys his his

 TTC TTG GTT GGT CTA CTT CTG AGG GAA ACT TCC ATT GCT CTT CAG GAC AAT TAT GAG ATC 3204
 phe leu val gly leu leu leu arg glu thr ser ile ala leu gln asp asn tyr glu ile

 AGA TAT ACA GCT ATC TCT GTT ATA AAG AAT CTT TTG ATA AAA CAT GCA TTT GAC ACA AGA 3264
 arg tyr thr ala ile ser val ile lys asn leu leu ile lys his ala phe asp thr arg

 TAC CAG CAC AAG AAC CAA CAA GCC AAA ATA GCA CAA TTG TAC CTC CCC TTT GTT GGA CTA 3324
 tyr gln his lys asn gln gln ala lys ile ala gln leu tyr leu pro phe val gly leu

 CTT TTG GAA AAT ATA CAG CGA TTA GCA GGT CGA GAT ACC TTG TAT TCT TGT GCA GCC ATG 3384
 leu leu glu asn ile gln arg leu ala gly arg asp thr leu tyr ser cys ala ala met

 CCT AAT TCT GCA TCC AGA GAT GAG TTT CCA TGT GGC TTT ACT TCA CCT GCC AAT AGA GGG 3444
 pro asn ser ala ser arg asp glu phe pro cys gly phe thr ser pro ala asn arg gly

 AGT CTG AGC ACT GAC AAA GAC ACC GCT TAT GGG TCT TTT CAA AAT GGA CAT GGA ATT AAG 3504
 ser leu ser thr asp lys asp thr ala tyr gly ser phe gln asn gly his gly ile lys

 AGA GAA GAT TCA AGA GGT TCC CTC ATC CCA GAA GGA GCA ACA GGA TTT CCA GAT CAG GGC 3564
 arg glu asp ser arg gly ser leu ile pro glu gly ala thr gly phe pro asp gln gly

 AAC ACT GGT GAA AAT ACC CGA CAG AGT TCT ACA AGG AGT AGT GTA TCC CAG TAT AAC CGC 3624
 asn thr gly glu asn thr arg gln ser ser thr arg ser ser val ser gln tyr asn arg

CTG GAT CAG TAT GAA ATC AGA AGC CTC CTG ATG TGC TAC CTG TAT ATA GTA AAA ATG ATT 3684
leu asp gln tyr glu ile arg ser leu leu met cys tyr leu tyr ile val lys met ile

TCA GAA GAT ACT CTC TTA ACT TAC TGG AAT AAA GTA TCA CCT CAG GAG CTC ATA AAC ATT 3744
ser glu asp thr leu leu thr tyr trp asn lys val ser pro gln glu leu ile asn ile

CTT ATA CTT TTA GAA GTA TGC TTG TTT CAC TTT AGA TAT ATG GGG AAA AGA AAC ATA GCA 3804
leu ile leu leu glu val cys leu phe his phe arg tyr met gly lys arg asn ile ala

AGG GTG CAT GAT GCC TGG CTG TCA AAA CAC TTC GGA ATA GAC CGA AAA TCG CAA ACC ATG 3864
arg val his asp ala trp leu ser lys his phe gly ile asp arg lys ser gln thr met

CCT GCT CTT CGA AAC AGA TCA GGA GTA ATG CAG GCC CGG CTT CAG CAT CTT AGT AGC CTA 3924
pro ala leu arg asn arg ser gly val met gln ala arg leu gln his leu ser ser leu

GAA AGT TCA TTT ACA CTT AAT CAC AGT TCT ACA ACA ACT GAA GCA GAC ATT TTC CAC CAG 3984
glu ser ser phe thr leu asn his ser ser thr thr thr glu ala asp ile phe his gln

GCA CTT CTT GAA GGC AAT ACA GCT ACT GAA GTT TCC CTA ACA GTA CTA GAC ACC ATA TCA 4044
ala leu leu glu gly asn thr ala thr glu val ser leu thr val leu asp thr ile ser

TTT TTC ACT CAG TGC TTC AAG ACC CAA CTT TTA AAT AAT GAT GGC CAT AAC CCA TTA ATG 4104
phe phe thr gln cys phe lys thr gln leu leu asn asn asp gly his asn pro leu met

AAA AAA GTG TTT GAT ATA CAT CTT GCT TTT CTT AAA AAT GGA CAA TCT GAA GTG TCG CTG 4164
lys lys val phe asp ile his leu ala phe leu lys asn gly gln ser glu val ser leu

AAA CAT GTA TTT GCC TCA CTG AGA GCT TTC ATC AGT AAG TTT CCT TCA GCA TTT TTC AAA 4224
lys his val phe ala ser leu arg ala phe ile ser lys phe pro ser ala phe phe lys

GGA AGA GTA AAC ATG TGT GCT GCA TTT TGC TAT GAG GTT TTA AAG TGC TGC ACA TCG AAG 4284
gly arg val asn met cys ala ala phe cys tyr glu val leu lys cys cys thr ser lys

ATT AGC TCA ACC AGG AAT GAA GCA TCT GCA CTT TTG TAT CTT TTG ATG AGA AAC AAC TTT 4344
ile ser ser thr arg asn glu ala ser ala leu leu tyr leu leu met arg asn asn phe

GAG TAT ACC AAA AGG AAA ACC TTT TTG AGG ACA CAT CTA CAG ATA ATA ATT GCT GTA AGC 4404
glu tyr thr lys arg lys thr phe leu arg thr his leu gln ile ile ile ala val ser

CAA CTG ATA GCT GAT GTA GCA CTA AGC GGA GGA TCA AGA TTT CAG GAG TCT TTA TTC ATT 4464
gln leu ile ala asp val ala leu ser gly gly ser arg phe gln glu ser leu phe ile

ATC AAT AAT TTT GCA AAT AGT GAC AGA CCT ATG AAG GCA ACT GCC TTT CCC GCA GAA GTC 4524
ile asn asn phe ala asn ser asp arg pro met lys ala thr ala phe pro ala glu val

AAA GAC TTG ACC AAG AGA ATC CGC ACT GTT CTT ATG GCC ACT GCC CAA ATG AAG GAG CAT 4584
lys asp leu thr lys arg ile arg thr val leu met ala thr ala gln met lys glu his

GAG AAA GAC CCT GAA ATG CTA ATT GAT CTC CAG TAT AGC TTA GCC AAG TCC TAT GCA AGC 4644
glu lys asp pro glu met leu ile asp leu gln tyr ser leu ala lys ser tyr ala ser

ACC CCA GAG CTC AGG AAA ACC TGG CTT GAT AGC ATG GCC AAG ATT CAT GTA AAA AAT GGA 4704
thr pro glu leu arg lys thr trp leu asp ser met ala lys ile his val lys asn gly

GAT TTT TCA GAG GCT GCG ATG TGT TAT GTC CAT GTA GCA GCT CTA GTT GCA GAG TTT CTT 4764
asp phe ser glu ala ala met cys tyr val his val ala ala leu val ala glu phe leu

CAT CGA AAA AAA TTA TTT CCT AAC GGA TGT TCA GCG TTC AAG AAA ATT ACT CCC AAT ATA 4824
his arg lys lys leu phe pro asn gly cys ser ala phe lys lys ile thr pro asn ile

GAT GAA GAA GGA GCA ATG AAA GAA GAT GCT GGG ATG ATG GAT GTC CAT TAT AGT GAA GAG 4884
 asp glu glu gly ala met lys glu asp ala gly met met asp val his tyr ser glu glu
 GTC TTG CTG GAG TTG CTA GAA CAA TGT GTG GAT GGC TTA TGG AAG GCA GAA CGT TAT GAA 4944
 val leu leu glu leu leu glu gln cys val asp gly leu trp lys ala glu arg tyr glu
 ATA ATT TCT GAG ATT TCC AAG TTG ATC GTT CCA ATT TAT GAG AAA CGT CGT GAG TTT GAG 5004
 ile ile ser glu ile ser lys leu ile val pro ile tyr glu lys arg arg glu phe glu
 AAA CTT ACT CAA GTT TAT AGA ACT CTT CAT GGA GCT TAC ACA AAA ATT CTG GAA GTT ATG 5064
 lys leu thr gln val tyr arg thr leu his gly ala tyr thr lys ile leu glu val met
 CAT ACA AAA AAG AGA CTT TTA GGC ACT TTC TTC AGA GTT GCC TTT TAT GGC CAA TCT TTT 5124
 his thr lys lys arg leu leu gly thr phe phe arg val ala phe tyr gly gln ser phe
 TTT GAA GAA GAA GAT GGA AAG GAG TAC ATC TAT AAA GAA CCA AAG CTC ACT GGC CTC TCA 5184
 phe glu glu glu asp gly lys glu tyr ile tyr lys glu pro lys leu thr gly leu ser
 GAA ATT TCC TTG AGA CTT GTT AAA CTT TAT GGT GAA AAG TTT GGT ACG GAG AAT GTC AAA 5244
 glu ile ser leu arg leu val lys leu tyr gly glu lys phe gly thr glu asn val lys
 ATA ATT CAG GAT TCA GAC AAG GTA AAT GCC AAA GAG CTT GAT CCA AAA TAT GCT CAT ATA 5304
 ile ile gln asp ser asp lys val asn ala lys glu leu asp pro lys tyr ala his ile
 CAA GTT ACT TAT GTG AAG CCT TAC TTT GAT GAC AAA GAA CTC ACA GAA AGG AAG ACC GAG 5364
 gln val thr tyr val lys pro tyr phe asp asp lys glu leu thr glu arg lys thr glu
 TTT GAA AGA AAT CAT AAT ATC AGC AGA TTT GTT TTT GAG GCC CCT TAC ACT TTA TCA GGC 5424
 phe glu arg asn his asn ile ser arg phe val phe glu ala pro tyr thr leu ser gly
 AAA AAA CAG GGC TGT ATA GAA GAA CAG TGC AAA CGC CGT ACA ATC TTG ACA ACT TCA AAC 5484
 lys lys gln gly cys ile glu glu gln cys lys arg arg thr ile leu thr thr ser asn
 TCG TTT CCT TAC GTG AAG AAG AGG ATT CCT ATT AAC TGT GAA CAG CAG ATT AAT TTA AAA 5544
 ser phe pro tyr val lys lys arg ile pro ile asn cys glu gln gln ile asn leu lys
 CCA ATT GAT GGT GCC ACT GAT GAA ATA AAA GAT AAA ACT GCA GAG CTG CAA AAG CTT TGC 5604
 pro ile asp gly ala thr asp glu ile lys asp lys thr ala glu leu gln lys leu cys
 TCC TCT ACT GAC GTG GAC ATG ATT CAG CTC CAA CTT AAA TTG CAG GGC TGG GTT TCT GTG 5664
 ser ser thr asp val asp met ile gln leu gln leu lys leu gln gly trp val ser val
 CAG GTC AAT GCT GGT CCA TTA GCA TAT GCA AGA GCT TTC TTA AAT GAC AGC CAA GCT AGC 5724
 gln val asn ala gly pro leu ala tyr ala arg ala phe leu asn asp ser gln ala ser
 AAG TAT CCA CCT AAG AAA GTG AGT GAG TTG AAA GAC ATG TTT AGG AAA TTT ATA CAA GCA 5784
 lys tyr pro pro lys lys val ser glu leu lys asp met phe arg lys phe ile gln ala
 TGC AGC ATT GCA CTT GAA CTA AAT GAG CGG CTA ATT AAA GAA GAT CAA GTT GAG TAC CAT 5844
 cys ser ile ala leu glu leu asn glu arg leu ile lys glu asp gln val glu tyr his
 GAA GGG CTA AAG TCA AAT TTC AGA GAC ATG GTA AAA GAA TTA TCT GAC ATT ATC CAT GAG 5904
 glu gly leu lys ser asn phe arg asp met val lys glu leu ser asp ile ile his glu
 CAG ATA TTA CAA GAA GAC ACA ATG CAT TCT CCC TGG ATG AGC AAC ACA TTA CAT GTA TTT 5964
 gln ile leu gln glu asp thr met his ser pro trp met ser asn thr leu his val phe

TGT GCA ATT AGT GGT ACA TCA AGT GAC CGA GGT TAT GGT TCC CCA AGA TAC GCT GAA GTG 6024
 cys ala ile ser gly thr ser ser asp arg gly tyr gly ser pro arg tyr ala glu val
 TGA GGA AAT GCA GAT GTA CGG TGA CAA TGA GAC TGA CCT TTC TCA GGA ATA TTT GGA GCT 6084
 OPA
 GTG CAA ATG TTA AAA TTT AAA GAT TTG ATA TAC ATG GAG TGT TTC TTC TCG ACA CCA AAA 6144
 TTT TCA TGT GTT CCA ACA GGG TGC TTA CAT ATT TGT AAA TAA GCA ACT TGA AAG TGC CTG 6204
 GAA AAT TGC ACC ACT GTG CTT GGT TTG TAC TTT TTT AGG TAA ATC TAT ATG CTG AAA AGT 6264
 AGA GCT CAA AAA CAG TAG TTC AAT TTG CTT AAT TAT TGC TTA AAA TAA TGG TAC TAT GTA 6324
 AAA TTG TAT AAT GGA ATA CAA TAA AAG GTA AAA ATT 6360